

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 25, 2006, 08:01:28 ; Search time 1540 Seconds
(without alignments)
9590.739 Million cell updates/sec

Title: US-10-521-811-1

Perfect score: 1202
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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:*

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16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1202	100.0	1228	8 US-10-437-963-20266	Sequence 20266, A
2	420	34.9	454	10 US-10-487-901-6995	Sequence 6995, Ap
3	375.2	31.2	1276	8 US-10-425-114-3220	Sequence 3220, Ap
4	375.2	31.2	1352	8 US-10-374-780A-568	Sequence 568, App
5	375.2	31.2	1352	8 US-10-412-6998-1061	Sequence 1061, Ap
6	372	30.9	1352	9 US-10-425-115-158957	Sequence 158957, A
7	366	30.4	1280	8 US-10-425-114-14357	Sequence 14357, A
8	366	30.4	1344	8 US-10-374-780A-564	Sequence 564, App
9	366	30.4	1344	8 US-10-412-6998-1057	Sequence 1057, Ap
10	352.6	29.3	1126	8 US-10-425-114-24903	Sequence 24903, A
11	352.6	29.3	1492	8 US-10-374-780A-567	Sequence 567, App
12	352.6	29.3	1492	8 US-10-412-6998-1060	Sequence 1060, Ap
13	345.6	28.8	815	9 US-10-425-115-39025	Sequence 39025, A
14	345.6	28.8	1400	9 US-10-425-115-38157	Sequence 38157, A
15	331.2	27.6	1084	8 US-10-374-780A-566	Sequence 566, App
16	331.2	27.6	1084	8 US-10-412-6998-1059	Sequence 1059, Ap
17	326.6	27.2	1074	3 US-09-443-704-3	Sequence 3, Appl

18	326.6	27.2	1074	6 US-10-008-118A-3	Sequence 3, Appl
19	324.6	27.0	777	8 US-10-437-963-90448	Sequence 90448, A
20	318.8	26.5	794	8 US-10-767-701-11055	Sequence 11055, A
21	315.6	26.3	1083	16 US-11-096-568A-25631	Sequence 25631, A
22	314.2	26.1	662	8 US-10-374-780A-565	Sequence 565, App
23	314.2	26.1	662	8 US-10-412-6998-1058	Sequence 1058, Ap
24	312.6	26.0	1086	8 US-10-425-114-1170	Sequence 1170, Ap
25	312.6	26.0	1088	9 US-10-425-115-151274	Sequence 151274, A
26	307.8	25.6	335	10 US-10-487-901-3480	Sequence 3480, Ap
27	302.8	25.2	643	8 US-10-374-780A-563	Sequence 563, App
28	302.8	25.2	643	8 US-10-412-6998-1056	Sequence 1056, App
29	296.8	24.7	866	9 US-10-425-115-27081	Sequence 27081, A
30	281.2	23.4	642	9 US-10-425-115-53108	Sequence 53108, A
31	278.8	23.2	577	3 US-09-443-704-37	Sequence 37, Appl
32	278.8	23.2	577	6 US-10-008-118A-37	Sequence 37, Appl
33	274.6	22.8	1467	16 US-11-096-568A-20587	Sequence 20587, A
34	271.8	22.6	777	8 US-10-374-780A-1542	Sequence 1542, Ap
35	271.8	22.6	777	8 US-10-412-6998-1636	Sequence 1636, Ap
36	269.2	22.4	1216	8 US-10-437-963-7945	Sequence 7945, Ap
37	249.8	20.8	804	8 US-10-437-963-68443	Sequence 68443, A
38	247.4	20.6	1116	8 US-10-437-963-55050	Sequence 55050, A
39	246	20.5	1212	8 US-10-437-963-39218	Sequence 39218, A
40	245.8	20.4	1023	8 US-10-437-963-84195	Sequence 84195, A
41	244.6	20.3	1285	8 US-10-425-114-31390	Sequence 31390, A
42	244.6	20.3	1285	9 US-10-425-115-75772	Sequence 75772, A
43	244.6	20.3	1302	8 US-10-374-780A-1543	Sequence 1543, Ap
44	244.6	20.3	1302	8 US-10-412-6998-1637	Sequence 1637, Ap
45	243	20.2	1427	6 US-10-021-811-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1
US-10-437-963-20266
Sequence 20266, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 20266
LENGTH: 1228
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_25649C.1
US-10-437-963-20266
Query Match 100.0%; Score 1202; DB 8; Length 1228;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAGCCGCTCCCTCCAGAACACACACGACAGAGACGAGCAGTTCAGATCAGAC 60
DB 24 CAGCCGCTCCCTCCAGAACACACACGACAGAGAGACGAGCAGTTCAGATCAGAC 83
QY 61 AGGGAAGAGCAAGCAACATGGGAGAGGCTCGTGTGGAGAAAGTGGGGCTCAAGAAG 120
DB 84 AGGGAAGAGCAAGCAACATGGGAGAGGCTCGTGTGGAGAAAGTGGGGCTCAAGAAG 143
QY 121 GGTTCATGACGCCGAGAGAGCAAGTCTCTGTCGCCCATATCCAGCGCCACGCGCAC 180

Db 144 GGTCCATGACGCGGAGAGAGCAAGTCTCTGTGCCACATCCAGGCCACCGGCCAC 203
Qy 181 GGCACCTGGCGGCCCTGCCCCAAGCAGCCGGCTGCTGCGGCAAGAGCTGCGCG 240
Db 204 GGCACCTGGCGGCCCTGCCCCAAGCAGCCGGCTGCTGCGGCAAGAGCTGCGCG 263
Qy 241 CTCGGGTGATCAACTACCTGGCGGCGGACATCAACCGGGGGCAACTCTTCCAAAGAGGAG 300
Db 264 CTCGGGTGATCAACTACCTGGCGGCGGACATCAACCGGGGGCAACTCTTCCAAAGAGGAG 323
Qy 301 GAGGACACCATCATCATCTCCACGAGCTGTTGGCAGAGGTGATCCGCAATTGCGCGC 360
Db 324 GAGGACACCATCATCATCTCCACGAGCTGTTGGCAGAGGTGATCCGCAATTGCGCGC 383
Qy 361 AGGTGCCCCGGAGAGAGCGAGCAACGAGATCAAGAACGTGTGGCACAACCACTCAAGAG 420
Db 384 AGGTGCCCCGGAGAGAGCGAGCAACGAGATCAAGAACGTGTGGCACAACCACTCAAGAG 443
Qy 421 CGCCTCGATGCGCGGCTGAGGGCGGCTCANTGTGCGGCGAGGGCGGCGAGAGCAAG 480
Db 444 CGCCTCGATGCGCGGCTGAGGGCGGCTCANTGTGCGGCGAGGGCGGCGAGAGCAAG 503
Qy 481 AAGCCGAGAGAGCGAGAGAGAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540
Db 504 AAGCCGAGAGAGCGAGAGAGAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 563
Qy 541 CGGTCCGCTCGTCTGCTGCTGAGCGAGTCTTGATGCTCTGCTGCTGCTGCTGCTGCT 600
Db 564 CGGTCCGCTCGTCTGCTGCTGAGCGAGTCTTGATGCTCTGCTGCTGCTGCTGCTGCT 623
Qy 601 GGCACACGCGGAGATCAGCTCGGCGTCCGCGTCCGCGTCCGCGAGAGAGAGAGCTCTTC 660
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Qy 661 ACCTCGGCTTCGAGAGAGTTCAGATCGACAGAGCTTCTGCTGCGAGAGCGCTGCTGATG 720
Db 684 ACCTCGGCTTCGAGAGAGTTCAGATCGACAGAGCTTCTGCTGCGAGAGCGCTGCTGATG 743
Qy 721 CGGCTGAGAGCGGTACGACTGTCATGAGAGCCCGGCGAGCGCTGCTGCTGCTGCTGCT 780
Db 744 CGGCTGAGAGCGGTACGACTGTCATGAGAGCCCGGCGAGCGCTGCTGCTGCTGCTGCT 803
Qy 781 GCGGACGATGAGACTGCTGCTGCGAGTTCATGAGAGTCCGCGAGAGCGAGAGCTGCTG 840
Db 804 GCGGACGATGAGACTGCTGCTGCGAGTTCATGAGAGTCCGCGAGAGCGAGAGCTGCTG 863
Qy 841 CCGGACATCTAGAGAGAGAGAGATTTTACCGTTCCTGCTGCTGCTGCTGCTGCTGCT 900
Db 864 CCGGACATCTAGAGAGAGAGAGATTTTACCGTTCCTGCTGCTGCTGCTGCTGCTGCT 923
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Qy 961 GGGAGATCAACAGAGAGAGAGAGAGAGATCAAGAGTGGATGCGATGAGAGAGAGAG 1020
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Qy 1021 TAGCTTGTAGTAAATTTCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1080
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Db 1104 ATCAGTATGAAAGCTGAGATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1163
Qy 1141 GGCTCGGCTTCTCATTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1200
Db 1164 GGCTCGGCTTCTCATTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1223
Qy 1201 AA 1202

Db 1224 AA 1225
RESULT 2
US-10-487-901-6995
; Sequence 6995, Application US/10487901
; Publication No. US20050091708A1
; GENERAL INFORMATION:
; APPLICANT: Oreido, Jeremiah Vincent
; APPLICANT: McCreary, David
; APPLICANT: Pell, Randy
; APPLICANT: Miller, Barbara
; APPLICANT: Wedgatz, Thadeus
; APPLICANT: Gachotte, Daniel
; APPLICANT: Blakeslee, Beth
; APPLICANT: Larrinua, Ignacio
; APPLICANT: Shukla, Vipula
; APPLICANT: Crosley, Rodney
; TITLE OF INVENTION: Nucleic Acid Compositions Confering Altered Metabolic Characteri
; FILE REFERENCE: DOM-08552
; CURRENT APPLICATION NUMBER: US/10/487,901
; NUMBER OF SEQ ID NOS: 7560
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6995
; LENGTH: 454
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-487-901-6995
Query Match 34.9%; Score 420; DB 10; Length 454;
Best Local Similarity 98.8%; Pred. No. 2.1e-111;
Matches 423; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 CAGCGGCTCCCTTCCAGAGACACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
Db 27 CAGCGGCTCCCTTCCAGAGACACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 86
Qy 61 AGGAG 120
Db 87 AGGAG 146
Qy 121 GGTCCATGAGAGCGCGAG 180
Db 147 GGTCCATGAGAGCGCGAG 206
Qy 181 GGCACCTGCGCGGCTCCGAG 240
Db 207 GGCACCTGCGCGGCTCCGAG 266
Qy 241 CTCGGGTGATCAACTACCTGCGCGGCGGAGATCAAGCGGGGCACTTCTCCAGAGAGAG 300
Db 267 CTCGGGTGATCAACTACCTGCGCGGCGGAGATCAAGCGGGGCACTTCTCCAGAGAGAG 326
Qy 301 GAGGACACCATCATCATCTCCACGAGCTGTTGGCAACAGGTGATCCGCAATTGCGCGC 360
Db 327 GAGGACACCATCATCATCTCCACGAGCTGTTGGCAACAGGTGATCCGCAATTGCGCGC 386
Qy 361 AGGTGCCCCGGAGAGAGAGAGAGAGAGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Db 387 AGGTGCCCCGGAGAGAGAGAGAGAGAGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 446
Qy 421 CGCCTCGA 428
Db 447 CGCCTCGA 454
RESULT 3
US-10-425-114-3220
; Sequence 3220, Application US/10425114

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/ Publication No. US20040034888A1
/ GENERAL INFORMATION:
/ APPLICANT: Liu, Jingdong
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Screen, Steven E
/ APPLICANT: Tabaka, Jack E
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(5313)B
/ CURRENT APPLICATION NUMBER: US/10/425,114
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 73128
/ SEQ ID NO 3220
/ LENGTH: 1276
/ TYPE: DNA
/ ORGANISM: Zea mays
/ FEATURE:
/ OTHER INFORMATION: Clone ID: 700243864_FLI
US-10-425-114-3220

Query Match          31.2%; Score 375.2; DB 8; Length 1276;
Best Local Similarity 64.6%; Pred. No. 3,7e-98;
Matches 711; Conservative 0; Mismatches 308; Indels 81; Gaps 7;

QY 76 ACAATGGGAGGGCTCGTCTGCGAGAAAGATGGGCTCAAGAGGCTCCATGACGCCG 135
DB 171 AGAATGGGAGAGCTCGTCTGCGAGAAAGATGGGCTCAAGAGGCGCATGAGACGCCG 230
QY 136 GAGGAGGAGAGGCTCTGCTCGGCCACATCCAGCGCCAGCGGCAACTGGCGCGCC 195
DB 231 GAGGAGGAGAGATCTGTGTCGCGACATCCAGAGTCTGGCCACAGCAACTGGCGCGG 290
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DB 351 TACCTGCGCGCGCATCAAGCGGGGCACTTCCAGAGAGAGAGAGACCGCATATC 410
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DB 411 ACCCTTCAGAGAGCTTCGCAACAGTGTGTCGCGCGCGCGCGCGCGCGCGG 470
QY 376 ACGGCAACGAGATCAAGAACTGTGGCACACCACTCAAGAGCGCTCGATGCGCC- 434
DB 471 ACGGCAACGAGATCAAGAACTGTGGCACACCACTCAAGAAAGCGCTGGAGCGCAC 530
QY 435 -----GCTCAGGGCGGTGATGTGCGCGCGAGCGGC 465
DB 531 ACCAAGCACTGAGAGAGAGAGACGAGCGGGGCGCATGAGTGTGACCGCGCAGAAG 590
QY 466 GCGCAAGAACACAGAAAGCGGAGAGCGGAGAAACCGCGCGCGCGCGCGCGCGG 525
DB 591 CCGAGAGAGCCCAAGCGCGCGGGGTGCGAGAGCAAGACGAGCGCGCGCGCGCGG 650
QY 526 CCGCGCTCGCGCGAGCGGTCCGCTCGTGTGCGTGTGCGAGTCTCGATGCGCTGTG 585
DB 651 GCGACACCGCGCGCGCGGTGCTGTAACGCTGCGCGCGCTCGTGTGCGAGCGAGT 710
QY 586 GTGGCGGAGAGAGACGCGCAACCGCGGATACGTCGCGCTCGCGCTGCTGTGCGCAAG 645
DB 711 ACGGAGACAGAGAGAGAGAAACAGGAGAGAGCT---CGCGCGGCTTCCCAAGAGAGAG 767
QY 646 GAGGAGAGCTCTTCACTCTGCGCTTCCGAGAGTTCAGATGAGACAGACAGCTTGTG 705
DB 768 AGCTTCACTTCTGCTTGTGAGGCGCGCGAGATTCAGTTCAAGACAGCTTCTGTG 827
QY 706 GAGACGCTGTGATGCGCTGTGACGCGGTACGAGC-----TGTC 744
DB 828 GAGAGCGCTGTGATGCGCTGTGACGCTTCAAGAGTCCCGACGAGCGCTCGACCTCC 887
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QY 745 ATGAGACCCGCGAGACCGCTTCTGTCGCGCGCCCATCCG-----CGAGCAG 789
DB 888 GCGCGTTCGCGGACACCTGCGCGCGCTCTCTCTCTGTCGTCGCGCGCGCGCAG 947
QY 790 ATGACTACTGCTGCGAGTGTTCATGAGATCCGCGGAGCG---CAAGCTTGGCGCAG 846
DB 948 TTGACTACTGCTGCGAGTGTTCATGAGATCCGCGGAGCGCGCACCAACACTGCGCAG 1007
QY 847 ATCTAGAG-----AAAGAGAGAAATTTTACCGTTCTTGGTTAATTGAT---TTGTT 897
DB 1008 GTTAAAGCGCGGACCGCGCGCGCGAGAAATTTTACGTTCTTGGTTAATTGAT 1067
QY 898 TTTTCTCTCTGTCGCGCGCATTTTGCACCGGAGGAGATAGCTAACGAGAGTGTCCA 957
DB 1068 CTTTCTCTCTCTGTCGCGCGCATTTTGCAGATTTGAGAGGAGACAGTCAATACAGC 1127
QY 958 TGAGCGAATCATCAACAGAGAAACGCGAATCATCATGATGCGATGAGATGACACC 1017
DB 1128 TAATTATAGAGGAGTGTGTGTGTGAGAGACACGACGAGATTAGAGAAACAGCGCA 1187
QY 1018 CAGTACCTTGAATGTAATTTTCTTTTAACTTCTCTGTATGTAAGAAACAGAA 1077
DB 1188 CATGCCATTGACATCTATCTGTGTGCTTCTTGTATATAAGATCATCATGACAA 1247
QY 1078 GAGATCAGTATCGAAACCT 1097
DB 1248 GATATCGTATCGAAACCT 1267

RESULT 4
US-10-374-780A-568
/ Sequence 568, Application US/10374780A
/ Publication No. US20040019927A1
/ GENERAL INFORMATION:
/ APPLICANT: Sherman, Bradley K
/ APPLICANT: Riechmann, Jose Luis
/ APPLICANT: Jiang, Cai-Zhong
/ APPLICANT: Heard, Jacqueline E
/ APPLICANT: Haake, Volker
/ APPLICANT: Creelman, Robert A
/ APPLICANT: Ratcliffe, Oliver
/ APPLICANT: Adam, Luc J
/ APPLICANT: Reuber, T. Lynne
/ APPLICANT: Keddie, James
/ APPLICANT: Brown, Pierre E
/ APPLICANT: Pilgrim, Marsha L
/ APPLICANT: Dubell III, Arnold T
/ APPLICANT: Pineda, Omaira
/ APPLICANT: Yu, Guo-Liang
/ TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
/ FILE REFERENCE: MBI-0047 CIP
/ CURRENT APPLICATION NUMBER: US/10/374,780A
/ CURRENT FILING DATE: 2003-02-25
/ PRIOR APPLICATION NUMBER: 09/837,944
/ PRIOR FILING DATE: 2001-04-18
/ PRIOR APPLICATION NUMBER: 60/310,847
/ PRIOR FILING DATE: 2001-08-09
/ PRIOR APPLICATION NUMBER: 09/934,455
/ PRIOR FILING DATE: 2001-08-22
/ PRIOR APPLICATION NUMBER: 60/336,049
/ PRIOR FILING DATE: 2001-11-19
/ PRIOR APPLICATION NUMBER: 60/338,692
/ PRIOR FILING DATE: 2001-12-11
/ PRIOR APPLICATION NUMBER: 10/171,468
/ PRIOR FILING DATE: 2002-06-14
/ PRIOR APPLICATION NUMBER: 10/225,066
/ PRIOR FILING DATE: 2002-08-09
/ PRIOR APPLICATION NUMBER: 10/225,067
/ PRIOR FILING DATE: 2002-08-09
/ PRIOR APPLICATION NUMBER: 10/225,068
/ PRIOR FILING DATE: 2002-08-09
/ NUMBER OF SEQ ID NOS: 2906
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Query Match	31.2%	Score 375.2;	DB 8;	Length 1352;
Best Local Similarity	64.6%	Pred. No. 3.8e-98;		
Matches 711; Conservative	0;	Mismatches 308;	Indels 81;	Gaps 77;

OY	76	ACAAATGGGAGGGGCTTCGTGCTCGGAGAAGATTGGGGCTTCAABAAGGTTCAATGAGCCGC	135
Db	195	AGAAATGGGAGAGGCTCCGTGCTCGAAGAAATGGGGCTTCAABAAGGGGGCACAAGCCGC	254
OY	136	GAGAGAGCAAGAGTGCTCTGTCGCCCAATTCAGAGCCACACGGCGCACGGCAACTGGAGCGCC	195
Db	255	GAGAGAGCACAGATCTCTGTCGCCCAATTCAGAGCTTGGGCCAACAGCAACTGGGGCGCG	314
OY	196	CTGCCCAAGCAAGCCGGGCTGCTGCTGCGGCAAGAGCTGCGGCTTCGGGTGATCAAC	255
Db	315	CTGCCCAAGCAAGCCGGGCTGCTGCGGTGCGGCAAGAGCTGCGGCTTCGGGTGATCAAC	374
OY	256	TACCTGGCGGCGGGAATCAAGGGGGGCAACTTCTCAAGAGAGAGAGAACCATCATC	315
Db	375	TACCTGGCGGCGGGAATCAAGGGCGGCAACTTCAACCAAGAGAGAGAGAGAGCCCATCATC	434
OY	316	CATCTCCACAGAGCTCTTGGCAACAGTGGTCCGGAATTGCGCGCAGAGTTGGCCCGGAGG	375
Db	435	AACCTCCACAGAGCTCTGCGCAACAGTGGTCCGCCATCGCGCGCAGAGCTGCCCGGGCGG	494
OY	376	ACGGAACAAGAGATCAAGAACGTGTGGCACACCACCTTCAGAGACGCTCGATGCGCC-	434
Db	495	ACGGAACAAGAGATCAAGAACGTGTGGCACACGCCACTTCAGAGACGCGCTGGAGCCACAC	554
OY	435	-----GGGTCAAGGGCGGCTCAATGTGCGCGCGGAGCGGC	465
Db	555	ACCAAGCAGCTGGAGCAGAGAGCAGACAGGGGGGCAATGACGTGTGACGCGCCACAGAG	614
OY	466	GGCAGAAGAGCACAAGAAAGCCGGAAGACGCGCAAGAAAGACAGCCGCGCGCCGCGCGC	525
Db	615	CGCAGCAAGGCCCAAGCGCGCGGGGTCCAGAGACGAAGAGAGAGCAGCGCGCGCTGCCCCG	674
OY	526	CCGGCGTGGCCCGAGCGGTCGCGCTCGTGTGCTGTGACGAGTCTTCATGGACTTCGTG	585
Db	675	GCCACCAACCGCGCCGCGCTGCTGTGAACGAGTCGGCGGCGCTCGTCTGCGATGACCAAGTCG	734
OY	586	GTCGGGAGAGAGCAGGCAAGCGCGGGAAATCAAGCTGGGGTCCGGGCTCGGTGAGCGCCAA	645
Db	735	ACGGAGCAGAGACAGGAGAAACACGGGAGACAGCT--CGCCCGGTTCCCCAAGAGAG	791
OY	646	GAGAGAGCTCTTCACTCGGCTTTCGAGAGATTCAGAGATTCAGACAGCTTCTGTGTCG	705
Db	792	AGCTTCACTCGTCTCTCGAAGGCGCCGAGAGATTCCAATTGACAGACAGTTCTGTGTCG	851
OY	706	GAGACGCTGTGATATCCGCTGAGCGGGTAACGACG-----TGTC	744
Db	852	GAGACGCTGTGATATCCGCTGAGCAGCTTCGACGACGTCCCACAGAGCCCTGACAGCTCC	911
OY	745	ATGGAGCCCGGAGACGCGTTCGTGCGCGCGGCATCGC-----GAGAGC	789
Db	912	GCGCGTTTCGGAGACGTGGCGCGCTCTCTCTCTCTCTCTCTCTGTCGTTGGCGCCGACCGCAG	971
OY	790	ATGGAATACTGAGCTCGAGATTTCAATGAGATCCGGCAGAGCG--CAAGACTTGGCCGAG	846
Db	972	TTGGACTACTGGCTCGAGATTTCAATGAAGTCCGGCGACCGGCACCAACATGCGCGCAG	1031
OY	847	ATCTAGAG-----AAAGAGAGAAATTTTACCGTTTCTTGGGTAAATTGAT--TTGTT	897
Db	1032	GTTTAGAGACGGCAGCGCGCGCCCGAGAAATTTTCACTTCTCTGGCTAAATTGATATCGTT	1091
OY	898	TTTTCTCTCTGCGCGCATCTTGCACGAGAGGACATAGCTAATCAGACAAGAGTGTCCA	957
Db	1092	CTTTCCTCTCTCCCTCAGCAGTCTTGCMAATCGGAATTCGAGAGGGAGACAGTCACAATGACAGC	1155
OY	958	TGAGCGAATCATCAAGCAGAAAGACGGGAATCATGCGATGCGATGCGATGAGATGACCC	1017
Db	1152	TAAATTAATAGAGGGGTGTGTGTGTGAGAGACACAGCAGATTTGAGAGAAACAACGGCA	1211

QY	1018	CAGNAGCTTTGATGATGTAATTTCTTTTTTAACTCCTTCTCTGATGTAATAGAAACGAA	1077
Db	1212	CATGCCATTCATCTATCTCTTGTTGCTCTTTGTGTATATTAAGATGATCGATCGACAA	1271
QY	1078	GAGATCAGTATCGAAACCT	1097
Db	1272	GATATCGGTGATCGAAACCT	1291

```

RESULT 6
US-10-425-115-158957
; Sequence 158957, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yinhua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 158957
; LENGTH: 1352
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_76543C.1
US-10-425-115-158957

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Query Match	30.9%	Score 372	DB 9	Length 1352
Best Local Similarity	65.0%	Pred. No. 3.2e-97		
Matches 714	Conservative 0	Mismatches 305	Indels 79	Gaps 8
Qy	76	ACAAATGGGAGGAGGCTCCGTCCTGCGAAMATGAGGGCTCAAGAAAGGCTCATGAGACGCC	135	
Db	197	AGAAATGGGAGAGGCTCCGTGCTCTGCGAAMATGGGGCTCAAGAGGGGGCCATGATGCCCG	256	
Qy	136	GAGGAGGACAAAGTCTCTGTCGCCACATCCAGCGCCACGGCCAACTGGAGCGCC	195	
Db	257	GAGGAGGACAAAGATCCGTGTCGCCACATCCAGAGCTTCGGCCACAGCAACTGGAGCGCGC	316	
Qy	196	CTGGCCAAAGAACGCCGGGCTGCTGCGTGTGGGGAGAAGGCTGCCGGCTCCGGTGGATTAAC	255	
Db	317	CTGGCCAAAGAACGCCGGGCTGCTGCGTGTGGGGAGAAGGCTGCCGGCTCCGTGGATTAAC	376	
Qy	256	TACCTGGGCGCGGACATCAAGCGGGGCACTTCTCCAAAGAGAGAGAGACACATCATC	315	
Db	377	TACCTGGGCGCGGACATCAAGCGGGGCACTTCAAGAGAGAGAGAGAGAGCGCATCATC	436	
Qy	316	CATCTCCAGAGCTGCTTGGCAACAGGTGTCCGCAATTGCCGCCAGGTTGCCGGAGG	375	
Db	437	ACCTTCACAGAGCAGCTCGGCAACAGGTGTCCGCCATCGCCGCCAGGCTGCCGGGCGG	496	
Qy	376	ACGGAACAACGATCAAGAACGTTGTGGCAACCCACTTCAAGAAAGGCCCTCATATC----	431	
Db	497	ACGGAACAACGATCAAGAACGTTGTGGCAACCCACTTCAAGAAAGGCCCTGAGGCCACCC	556	
Qy	432	-----GCCGGCTCAGAGGCGGTCAATGTCGCGGCGAGAGCGGCGCAAGAAAG	474	
Db	557	ACCAAGACGCTGGAGCGAGGACAGACACGGGGCGCATTCAGATGTGTACGCCGCCCAAGAAAG	616	
Qy	475	CACAAAGAGCCGAAGAGCGG-----AAGAAAGCAAGCCGCCGCCGCCGCCGCCGCC	527	
Db	617	CGAGACAGGCCCAAGCGCGCGGGTGCAGGAAGAACGACGACGCGCGCGCTCGCCCGCGG	676	
Qy	528	GGCGTCGCCCGGAGCGGTCGCCCTCTGCTGTGTGGTGAAGAGTCTTCAATGACCTTCGTGCT	587	
Db	677	CACACACGCGCCCGGCGCTGCTTGAACGCTGTGGGGCGCTCGTCTGTGGTGAACCAAGTCGAC	736	
Qy	588	GGCGGAGGAGCACGGCAACCGCGGAGTCAAGTCCGGCGTCCGCGCTCGTGTGCGCCCAAGGA	647	


```

; GENERAL INFORMATION:
; APPLICANT: Sherman, Bradley K
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Heard, Jacqueline E.
; APPLICANT: Haake, Volker
; APPLICANT: Creelman, Robert A
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Adam, Luc J
; APPLICANT: Reuber, T. Lynne
; APPLICANT: Keddie, James
; APPLICANT: Brown, Pierre E
; APPLICANT: Pilgrim, Marsha L
; APPLICANT: Dubell III, Arnold T
; APPLICANT: Pineda, Omaira
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
; FILE REFERENCE: MBI-0047 CIP
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: US/10/374,780A
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/310,847
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/934,455
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/336,049
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/338,692
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: 10/171,468
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 10/225,066
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/225,067
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/225,068
; PRIOR FILING DATE: 2002-08-09
; NUMBER OF SEQ ID NOS: 2906
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 564
; LENGTH: 1344
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Predicted polypeptide sequence is orthologous to G241
US-10-374-780A-564

Query Match      30.4%; Score 366; DB 8; Length 1344;
Best Local Similarity 65.7%; Pred. No. 1.8e-95;
Matches 706; Conservative 0; Mismatches 270; Indels 98; Gaps 8;

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```

; GENERAL INFORMATION:
; APPLICANT: Sherman, Bradley K
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Heard, Jacqueline E.
; APPLICANT: Haake, Volker
; APPLICANT: Creelman, Robert A
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Adam, Luc J
; APPLICANT: Reuber, T. Lynne
; APPLICANT: Keddie, James
; APPLICANT: Brown, Pierre E
; APPLICANT: Pineda, Omaira
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Samana, Raymond R.
; APPLICANT: Pilgrim, Marsha L.
; APPLICANT: Creelman, Robert A.
; APPLICANT: Dubell, Arnold N.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
; FILE REFERENCE: MBI-0047 CIP
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: US/10/374,780A
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/310,847
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/934,455
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/336,049
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/338,692
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: 10/171,468
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 10/225,066
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/225,067
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/225,068
; PRIOR FILING DATE: 2002-08-09
; NUMBER OF SEQ ID NOS: 2906
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 564
; LENGTH: 1344
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Predicted polypeptide sequence is orthologous to G241
US-10-374-780A-564

Query Match      30.4%; Score 366; DB 8; Length 1344;
Best Local Similarity 65.7%; Pred. No. 1.8e-95;
Matches 706; Conservative 0; Mismatches 270; Indels 98; Gaps 8;

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OY	136	GAGGAGGAGCAAGAGTCTCGTCCGACATTCAGAGCGCAAGGCAAGGCAACCTGGGCGCGC	195
Db	134	GAGGAGGAGCAAGAGTCTCGTCCGACATTCAGAGCTTGGGCAAGCACTGGGCGCGG	193
OY	136	CTGCCAAGCAAGCCGGGCTGCTGGCTTTCGGCAAGAGCTGCGGCTCCGATGATCAAC	255
Db	134	CTGCCAAGCAAGCCGGGCTGCTGGGATGCGGCAAGAGCTGCGGCTCCGATGATCAAC	253
OY	256	TACCTGCGGCGGACATCAAGCGGGGCAACTTCTCCAAGAGAGAGAGCAACATCATC	315
Db	254	TACCTGCGGCGGACATCAAGCGCGGCAACTTCAGCAGAGAGAGAGAGCAATCATC	313
OY	316	CATCTCCACGAGCTGCTGGCAACAGATGATCGCAATTGGCCGCAAGTTGGCCGGAGG	375
Db	314	AGCCTTCACGAGCAGCTCGGCAACAGTGTGCTCCGATCGCCGCAAGCTTGGCCGGCGG	373
OY	376	ACGGAACAAGAGATCAAGAAGCTGTGGCAACCCCACTTCAGAAAGCGCTCGATGC---	431
Db	374	ACGGAACAAGAGATCAAGAAAGTGTGGCAACGCAACTTCAGAAAGCGCTCGATCCACC	433
OY	432	-----GCCGCTCAGGGCGGATCATGTCCGGCGAAGCGGGCGGCAAGAACAC	477
Db	434	AAGCAGAGCAGCACACGACGACGAGGAGCAGCGCGCGCTGGCGCGCAAGAACAC	493
OY	478	AAGAAGCCGAAGAGCGCGAAG-----AAGCCA	504
Db	474	AGGCCCCGACGCGCGGCGAAGCGCGGGGGCGGCGAGCCAGGAAGCCAGCGCCAAAGCC	553
OY	505	GCCGCTGTC-----G	555
Db	554	GACGCGCTGTGTGTGCTCCGGCCCCGGCCCCGGGACCGCTGGCGCGCGGCTCCGACGG	613
OY	556	TCGGTGAAGGAGTCTTCGATGGCTCTGTGCTGTGGGAGAGAACAGGCAAGCGCGGATC	615
Db	614	TCGGGCGCTCTCTGTGTGGTGAACGAGTGTTCATGACGAGCAAGACAGGAGACGAGC	673
OY	616	AGCTCGGCGTCCGCGCTCGGTGCGCCCAAGAGAGAGAG-----CTCCTTCACTCGGCT	669
Db	674	AACACGGGGAGGTGCGCGCGCGCTTCCCAAGAGAGAGAGCTTCAACAATCTCTCTCGGAC	733
OY	670	TCCGAGAGTTCAGATGACGACAGACTTGTGTGAGAGAGCGCTGTCAATGCGCTGGA-	728
Db	734	GCCGAGGAGTTCAGATTCGACGACAGCTTGTGTGCGAGAGCGCTGTCAATGCGCTGGA-	793
OY	729	-----CGGATACGAGGTGCTCATGAGCGCCGGCGAG-----	760
Db	794	AGCCTCGACGAGCTGTCCCAATGAGGCTTCCGACGACGACGCGTTCGGCGAGCTGCAC	853
OY	761	-----CGTTCGTCGCGCGGCGCATCCGCGCAGACGACATGAGCTACGCTCGGA	807
Db	854	GTGGCTGCGCGCTCTCTCTCTGTCGTCGGCGCGGCGGCGGACGCTGAGCTACGCTTCAGA	913
OY	808	GTTGTTCAATGAGTCCGGCGGAAGCGCA---AGACTTCCGCGAGATCTAAGAAAGAGAG	864
Db	914	GTTGTTCAATGAGTCCGGCGGACGCGCACCAAGAACTGCGCGAGATTTAAGCCGCTGCGCG	973
OY	865	AATTTCACGTTCTTGGGTTAAT-----TGAATTGTTTTCTCTCTGCGGCATCT	919
Db	974	AGAAATTTTCGGCTCTTAATTGATTTATGCTTTTGTCTCTATCTCTCTGCAAGCTT	1033
OY	920	TGCACCGGAGGACATAGCTAAACAGACAGAAGTGTCAATGAGCAATATCAAGCAGAA	979
Db	1034	TGCATTCGAGGGGAGCAGCAAGAGACGACGACGTCGATTTAACAGAGAAAGAAATAGGCA	1093
OY	980	GAA	982
Db	1094	GAA	1096

RESULT 11
US-10-374-780A-567
; Sequence 567, Application US/10374780A
; Publication No. US20040019927A1

```

: GENERAL INFORMATION:
: APPLICANT: Sherman, Bradley K
: APPLICANT: Riechmann, Jose Luis
: APPLICANT: Jlang, Cai Zhong
: APPLICANT: Heard, Jacqueline E
: APPLICANT: Haake, Volker
: APPLICANT: Creelman, Robert A
: APPLICANT: Ratcliffe, Oliver
: APPLICANT: Adam, Luc J
: APPLICANT: Reuber, T. Lynne
: APPLICANT: Keddie, James
: APPLICANT: Brown, Pierre E
: APPLICANT: Pilgrim, Marsha L
: APPLICANT: Dubell III, Arnold T
: APPLICANT: Pineda, Omaira
: APPLICANT: Yu, Guo-liang
: TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
: FILE REFERENCE: MBI-0047 CIP
: CURRENT APPLICATION NUMBER: US/10/374,780A
: CURRENT FILING DATE: 2003-02-25
: PRIOR APPLICATION NUMBER: 09/837,944
: PRIOR FILING DATE: 2001-04-18
: PRIOR APPLICATION NUMBER: 60/310,847
: PRIOR FILING DATE: 2001-08-09
: PRIOR APPLICATION NUMBER: 09/934,455
: PRIOR FILING DATE: 2001-08-22
: PRIOR APPLICATION NUMBER: 60/336,049
: PRIOR FILING DATE: 2001-11-19
: PRIOR APPLICATION NUMBER: 60/338,652
: PRIOR FILING DATE: 2001-12-11
: PRIOR APPLICATION NUMBER: 10/117,468
: PRIOR FILING DATE: 2002-06-14
: PRIOR APPLICATION NUMBER: 10/225,066
: PRIOR FILING DATE: 2002-08-09
: PRIOR APPLICATION NUMBER: 10/225,067
: PRIOR FILING DATE: 2002-08-09
: PRIOR APPLICATION NUMBER: 10/225,068
: PRIOR FILING DATE: 2002-08-09
: NUMBER OF SEQ ID NOS: 2906
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 567
: LENGTH: 1492
: TYPE: DNA
: ORGANISM: Zea mays
: FEATURE:
: OTHER INFORMATION: Predicted polypeptide sequence is orthologous to G241
: US-10-374-780A-567

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	Query Match	Similarity	29.3%;	Score 352.6;	DB 8;	Length 1492;
	Best Local	Similarity	66.8%;	Pred. No. 1.5e-91;		
	Matches	683;	Conservative	0;	Mismatches 224;	Indels 116; Gaps 8;
Oy	76	ACATGGGGAAGGGCTCCGTGCTGGAGAAGATGGGGCTCAAGAAGGGTCCATGAGCGCG				135
Db	119	ATATGGGGAAGGGCTCCGTGCTGCGAAGATGGGGCTGAAGAAGGGGCCATGAGCGCC				178
Oy	136	GAGAGGACAAGGTCTCTGTGCGCCACATCCAGCGCCACGGCCACCTGCGCGCC				195
Db	179	GAGAGGACAAGGTCTGTGTCGCCACATCCAGAGCTTCGGCCACACGACTGGCGGCG				238
Oy	196	CTGCCCCAAGCAGCGCGGCTGTCTGCTGGCGCAAGAGCTTCGGCTCCGTGATCAAC				255
Db	239	CTGCCCAAGCAGCGCGGCTGTCTGCTGGCGCAAGAGCTTCGGCTCCGTGATCAAC				298
Oy	256	TACCTGGGGCGGACATCAAGCGGGGGAACCTTCTCCAAGAGAGGAGGACACCATCATC				315
Db	299	TACTGGCGCCCGGACATCAAGCGGGGAACCTTCAGCAAGAGAGGAGGACGCCATATC				358
Oy	316	CATCTCAGCAGGTCTTGGCAACAGGTGTTCGCAATTCGCGCAGGTTGCCCGGAGG				375
Db	359	AGCTTCACAGCAGCTCTCGGCACAGGTGTGTCCGCATTCGCGCGCAGGCTGCCCGGCG				418
Oy	376	ACGGACAACGATCAAGAAAGTGTGGCACACCCACTTCAAGAAAGCGCTCGATGC----				431

Db 599 GAGCGGTGTGTCCTCCGCGCCCGGCGCCAGCGCTGCGCGGCGTCTCCCGAAGC 658
Qy 556 TCGGTGACGAGAGTCTCTGATGCGCTGTGTCGCGAGAGACGCGCAACGCGGAGATC 615
Db 659 TCGGCGCGCTCGTCTGCGGTGACCGAGTCGTCATACGAGACGAGACGAGCAGCGG 718
Qy 616 AGCTGGCGCTCGCGCTGTCGTCGCGCAAGAGAGAG-----CTCCCTTCACTCGGCT 669
Db 719 AACACGGGAGAGCTCGCGCGGTCCTCCAGAGAGAGAGCCTCACACCTCTCTCGGAC 778
Qy 670 TCGAGAGAGTTCAGATTCAGACGACGCTTCTGTCGAGAGCGCTGTCGATGCGCTGGA- 728
Db 779 GCGAGGAGATTCAGATTCAGACGACGCTTCTGTCGAGAGCGCTGTCGATGCGCTGGA- 838
Qy 729 -----CGGTACGACGCTGTCATGAGAGCGCGGAGC----- 760
Db 839 AGCCTGACGACGCTCTCCCATGAGAGCCTCCGACGACGCGTTCGCGAGCTCGAC 898
Qy 761 -----CGTTCGTCGCGCGCCCATCGCGAGACATGAGACTTACTGCGTCCGA 807
Db 899 GTGGCTCGCGCTCTCTCTGTCGTCGCGCGCGAGCGGACCTGAGACTTACTGCTCAGA 958
Qy 808 GTGTCATGAGAGTCCGCGAGAGCGCA---AGACTTCCGCGAGATCTAGAGAAAGAGAG 864
Db 959 GTGTCATGAGAGTCCGCGAGAGCGGACCGAGACCGAGACTCCGAGATTAGACCGCTCGCG 1018
Qy 865 AATTTTACCGTTCCTTCTGCTTAT-----TGATTTGTTTTTCTCTCTGCGCGCATCT 919
Db 1019 AGAATTTTCCGCTCTTAATTGATTGATTCGTTCTTTGTCCTTCTCTCTGACGCTCT 1078
Qy 920 TGCACCGGAGGACATAGCTAACAGACAGAGTGTCCATGAGGATCATCAAGAGAA 979
Db 1079 TGCATCGAGGAGGACGAGACAGACAGAGCTGATTAAAGAGAAAGAAATCAGGA 1138
Qy 980 GAA 982
Db 1139 GAA 1141

RESULT 13

US-10-425-115-39025
; Sequence 39025, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 39025
; LENGTH: 815
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_135592C.1
US-10-425-115-39025

Query Match 28.8%; Score 345.6; DB 9; Length 815;
Best Local Similarity 70.8%; Pred. No. 1.3e-89;
Matches 459; Conservative 0; Mismatches 189; Indels 0; Gaps 0;

Qy 61 AGGGAAGGAGCAAGCAATGGGGAGGCTCGCTGTGAGAGATGGGGCTCAAGAG 120
Db 146 AAGGAGAGAGAGCGGTAATGGGAGGCTCGCTGTGAGAGATGGGGCTCAAGAG 205
Qy 121 GGTTCATGACCGCGAGAGAGCAAGTCTCTGTCGCCACATCCAGCGCCACGCGCAC 180

Db 206 GGCCCTGAGACGCGGAGAGAGCAAGATCTGTGCGCCACATCCAGAGCCAGCGCAC 265
Qy 181 GCGAATCGCGCGGCTTCTGCCAAGACCGGCTCTGCTGTGCGGCAAGAGCTCCG 240
Db 266 GCGAATCGCGCGGCTTCTGCCAAGAGCGGCTCTGCTGTGCGGCAAGAGCTCCG 325
Qy 241 CTCGGGTGATCAACTACCTGCGGCGGAGCATCAAGCGGAGCAACTTCTCAAGAGAG 300
Db 326 CTCGGGTGATCAACTACCTGCGGCGGAGCATCAAGCGGAGCAACTTCTCAAGAGAG 385
Qy 301 GAGGACCATCATCATCTCCACGAGCTGTTGGCAAGAGTGTCTCCGAATTGCGCGC 360
Db 386 GAGCATCATATCATCCAGTGCACAGCTGCTCGGACAGATGTCCGGATTGCGCGC 445
Qy 361 AGGTTCCCGGAGAGACGAGCAACGAGATCAAGAACGTGTGGACACCCACTCAAGAG 420
Db 446 CGGCTGCGGAGAGAGAGCAACGAGATCAAGAACGTGTGGACACCCACTCAAGAG 505
Qy 421 CGCTGATGCGCGGCTGAGGCGGCTCATGTGCGCGGAGCGGCGGCAAGAGACAG 480
Db 506 CGCTGATGCGCGGCTGAGGCGGCTCATGTGCGCGGAGCGGCGGCAAGAGACAG 565
Qy 481 AAGCGAAGAGCGCGAAGAGCCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540
Db 566 AAGCG 625
Qy 541 CGGTCGCTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 600
Db 626 TGACCGCGCAAGCG 685
Qy 601 GCGAAGCGCGGATGAGCTCGGCGTCCGCGTCCGTCGTCGTCGTCGTCGTCGTCGTC 660
Db 686 ACCGATCAGTCACCGCGCTCGGTCGCGGAGAGACAGACAGGACACTTCGCGAGCTTC 745
Qy 661 ACCTCGCTTCGAGAGATTCAGATCGACGACGCTTCTGTGCGAG 708
Db 746 GCGTCGCTTCG 793

RESULT 14

US-10-425-115-38157
; Sequence 38157, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 38157
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_134802C.1
US-10-425-115-38157

Query Match 28.8%; Score 345.6; DB 9; Length 1400;
Best Local Similarity 70.5%; Pred. No. 1.6e-89;
Matches 550; Conservative 0; Mismatches 164; Indels 66; Gaps 4;

Qy 76 ACAATGGGAGGCTCCGTCGTCGAGAAAGATGGGGCTCAAGAGAGTCCATGACGCGC 135
Db 117 ATTAATGGGAGGCTCCGTCGTCGAGAAAGATGGGGCTCAAGAGAGGCGCATGACGCGC 176
Qy 136 GAGAGAGCAAGAGTCTCTGTCGCCACATCCAGCGCCACGCGCACGCTGCGCGCC 195
Db 177 GAGAGAGCAAGAGTCTCTGTCGCCACATCCAGAGCTTCCGCGCACGCAACTGCGCGCG 236


```

Qy      739 GT-----GTCATGAGCCCGCGACCGCTTCGTGGCCG 774
Db      802 TTCAGTCCGGGTGAGCAGCGGAGGCGAGCTTCGCGCGCGCGCGCGCGCGCG 861
Qy      775 CCATCGCGCGAGCATGACTACTGAGCTCGAGTGTTCATGAGTCCGCGAAGCGCA 834
Db      862 TCGACCAAGCAGCATGACTTCTGCTCAAGCTGTTCAATGAGGCGAAGCATGCA 921
Qy      835 GACTTGCCGCGAGT 848
Db      922 AATTGCCCGAGT 935

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Search completed: June 25, 2006, 09:58:37
 Job time : 1548 secs

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No.	Score	Match	Length	DB	ID	Description
1	201.4	16.8	766	3	US-09-640-211A-2027	Sequence 2027, AP
2	199.8	16.6	648	3	US-09-640-211A-2036	Sequence 2036, AP
3	195.8	16.3	1344	2	US-08-722-62EB-1	Sequence 2036, AP
4	193.6	16.1	1046	3	US-09-533-02B-61	Sequence 1, Appl
5	193.4	16.1	1424	3	US-09-640-211A-1965	Sequence 61, Appl
6	192.6	16.0	563	3	US-09-640-211A-252	Sequence 1965, AP
7	190.8	15.9	360	3	US-09-640-211A-1266	Sequence 252, Appl
8	190.8	15.9	513	3	US-09-640-211A-519	Sequence 1266, AP
9	188	15.6	631	3	US-09-640-211A-1718	Sequence 519, Appl
10	188	15.6	1150	3	US-09-640-211A-2088	Sequence 1718, AP
11	181.6	15.1	1473	3	US-09-640-211A-2087	Sequence 2088, AP
12	181.6	15.1	1576	3	US-09-640-211A-2105	Sequence 2087, AP
13	181.2	15.0	636	3	US-09-640-211A-1797	Sequence 2105, AP
14	180	15.0	509	3	US-09-640-211A-1982	Sequence 2105, AP
15	179	14.9	373	3	US-09-640-211A-2071	Sequence 1797, AP
16	179	14.9	373	3	US-09-640-211A-1981	Sequence 1982, AP
17	178.4	14.8	311	3	US-09-640-211A-181	Sequence 2071, AP
18	178.4	14.8	311	3	US-09-640-211A-189	Sequence 181, Appl
19	177.4	14.8	385	3	US-09-640-211A-2057	Sequence 2891, AP
20	173.4	14.4	564	3	US-09-640-211A-1987	Sequence 1499, AP
21	170	14.1	476	3	US-09-640-211A-2020	Sequence 2057, AP
22	165.6	13.8	361	3	US-09-640-211A-1684	Sequence 2020, AP
23	162.6	13.5	2352	3	US-08-997-251-3	Sequence 1987, AP
						Sequence 1684, AP
						Sequence 3, Appl

Qy	34	CCGCATTTCGCGCAGGTGGCCCCGGGAGGACGACAAAGATCAAGAACCTTGCGACA	406
Db	540	CGGTATAGCGGACCGTTGCCGGGAGGACGACAAAGATTAAAGACTTAATCGAACA	599
Qy	407	CCCACCTCAAAGAGCGCTTCGATGGCG	433
Db	600	CCACATCAAGAAGAAAGTTCAAGCAC	626

RESULT 2

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US-09-640-211A-2036
Sequence 2036, Application US/03640211A
Patent No. 6833446
GENERAL INFORMATION:
APPLICANT: Wood, Marion
APPLICANT: Sheink, Michael A.
APPLICANT: McGrath, Annette
TITLE OF INVENTION: Compositions and Methods for the Treatment of Gene
FILE REFERENCE: 11000.1021CIU
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
SOFTWARE: PasteSeq for Windows Version 4.0
SEQ ID NO 2036
LENGTH: 648
TYPE: DNA
ORGANISM: Eucalyptus grandis
US-09-640-211A-2036

```

Query Match	16.6%	Score 199.8;	DB 3;	Length 648;
Best Local Similarity	73.5%;	Pred. No. 6.5e-33;		
Matches 255; Conservative	0;	Mismatches 92;	Indels 0;	Gaps 0

QY	7	ATGGGAGGAGCTCCGCTGCGAGAAAGATGGGGCTCAAGAAAGGTCATGGACCGGAG	138
QY	72	ATGGGAGGCGAACCGTGTCTGTACAATTCGGGGGTGAAGAAAGACCGTGGACCGCGGAG	131
QY	139	GAGGACAAAGTCTCTGTGCGCCACATCCAGCGCCACGGCCACGGCACTGGCGCGCTTG	198
Db	132	GAGGACAAAGCTATCAACTTCAATCTTCACCAACGGCCACTGCTGTGGCGTGGCCGTC	191
QY	199	CCCAAGCAAGCGGGGCTGCTGCTTGGCGGCAAGAGCTCCGAGTCCGGTGGATCAACTAC	258
Db	192	CCTAAGCTTGGCGGCTCGCGCGCTGGCGGCAAGAGCTCCGCTCCGTGGACCAACTAC	251
QY	259	CTGCGGCCGGAATCAAGCGGGGCACTTCTTCAAAGAGAGAGAGACATCATATCAT	318
Db	252	CTCCGCGCCGACCTCAAGCGGCGCTCTCTCACTGAGGTGAGGAGACAGCTGTATGAC	311
QY	319	CTTCCAGAGCTGTTGGCAACAGTGTGTCCGCAATTTGCGGCAGATTTGCCCGGAGAGCG	378
Db	312	CTCTCATGTCCCGCTCGGCAACAGTGTGTGAAAGATTCGGCGCAAGTTGCCCGGGAGAAC	371
QY	379	GACAAAGAGATCAAGAACTGTGGCAACGCCACTTCAGAAAGCGCT	425
Db	372	GACAAAGAAATTAAGAACCATTTGAAACCCACATTCAGAAAGAACT	418

RESULT 3

US-08-722-626B-1
 / Sequence 1, Application US/08722626B
 / Patent No. 5939601
 /
 / GENERAL INFORMATION:
 /
 / APPLICANT: Yang, Yinnong
 / APPLICANT: Kleesig, Daniel, F.
 / TITLE OF INVENTION: NOVEL GENES ASSOCIATED WITH ENHANCED
 / TITLE OF INVENTION: DISEASE RESISTANCE IN PLANTS
 / NUMBER OF SEQUENCES: 9
 /
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Dann, Dorfman, Herrell and Skillman
 / STREET: 1601 Market Street Suite 120

```

1      CITY: Philadelphia
2      STATE: PA
3      COUNTRY: USA
4      ZIP: 19103-2307
5      COMPUTER READABLE FORM:
6      MEDIUM TYPE: Diskette
7      COMPUTER: IBM Compatible
8      OPERATING SYSTEM: DOS
9      SOFTWARE: FastSeq Version 1.5
10     CURRENT APPLICATION DATA:
11     APPLICATION NUMBER: US/08/722,626EE
12     FILING DATE: 27-SEP-1996
13     CLASSIFICATION: 800
14     PRIOR APPLICATION DATA:
15     APPLICATION NUMBER:
16     FILING DATE:
17     ATTORNEY/AGENT INFORMATION:
18     NAME: Pat Hagan
19     REGISTRATION NUMBER: 27,643
20     REFERENCE/DOCKET NUMBER: 97-0010
21     TELECOMMUNICATION INFORMATION:
22     TELEPHONE: 215 563-4100
23     TELEFAX: 215 563-4044
24     TELEX:
25     INFORMATION FOR SEQ ID NO: 1:
26     SEQUENCE CHARACTERISTICS:
27     LENGTH: 1344 base pairs
28     TYPE: nucleic acid
29     STRANDEDNESS: single
30     TOPOLOGY: linear
31     MOLECULE TYPE: cDNA
32     HYPOTHEICAL: NO
33     ANTI-SENSE: NO
34     FRAGMENT TYPE:
35     ORIGINAL SOURCE:
36     FEATURE:
37     NAME/KEY: Coding Sequence
38     LOCATION: 148...981
39     OTHER INFORMATION:
40
41 US-08-722-626B-1

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Query Match	16.3%;	Score 195.8;	DB 2;	Length 1344;
Best Local Similarity	71.6%;	Pred. No. 5.3e-32;		
Matches 257; Conservative	0;	Mismatches 102;	Indels 0;	Gaps 0;

QY	72	AAGCAAAATGGGGAGAGGGCTCCGTCGTGGAAAGATGGGGCTCAAGAAAGGTCATGGAC	131
Db	141	AAGAAATATGGTGAAGAGCTCTTGTGTGGAAAAATGGGCTGAAAAAAGGCGCAATGGAT	200
QY	132	GGCGAGAGAGCAAGATCTCTGTGGCCATCAGCGCCAGCGCACCGGCAACTGGCG	191
Db	201	TCTGTAGAAAGATCAAGATTCTCATCTCTTTCATTCAAACTAATGGCCATGGCAACTGGCG	260
QY	192	CGCCCTGCCAAGCAAGCGGGCGTGTGCGGCAAGAGCTGCCGGCTCCGGTGGAT	251
Db	261	AGCGCTTCCCAAAGAGCGCTGGACTAATTAGATGCGGGAGAGTTGCAAGCTGGGTGGAC	320
QY	252	CAACTACTCTGGCGCGGACATCAAGCGGGGCACTTCTCCAGAGAGAGAGACACAT	311
Db	321	GAAATATTTGGCACCGAGATATAAAGAGGGGAAATTTCCACAGAGAMAMAMAAACAAT	380
QY	312	CATTCATCTCCACGAGCTGTGTGGCAACAGTGGTCCGCAATTGCCAGTGTGGCCGG	371
Db	381	TATCCAGTTACATGTAAGATGGCTTGGCAATAGTGTGTGCAATAGCAGCAAAATTAACAGG	440
QY	372	GAGGACGAGCAACGAGATCAAGAAAGTGTGGCAACCCACCTCAAGAGCGCTCTGAT	430
Db	441	ACGACAGACATGAAATTAATAAATGTTTGGCAACCCACTTGAGAGAGAAAGCTCAAG	499

RESULT 4

US-09-533-029-61
; Sequence 61, Application US/09533029

```
/ Patent No. 6664446
/ GENERAL INFORMATION:
/ APPLICANT: Heard, Jacqueline
/ APPLICANT: Broun, Pierre
/ APPLICANT: Riechmann, Jose-Luis
/ APPLICANT: Keddie, James
/ APPLICANT: Pineda, Omartra
/ APPLICANT: Adam, Luc
/ APPLICANT: Samaha, Raymond
/ APPLICANT: Zhang, James
/ APPLICANT: Yu, Guo-Liang
/ APPLICANT: Ratcliffe, Oliver
/ APPLICANT: Pilgrim, Marsha
/ APPLICANT: Jiang, Cai-Zhong
/ APPLICANT: Reuber, Lynne
/ TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES
/ FILE REFERENCE: MBI-010
/ CURRENT APPLICATION NUMBER: US/09/533,029
/ EARLIER FILING DATE: 2000-03-22
/ EARLIER APPLICATION NUMBER: 60/125,814
/ EARLIER FILING DATE: 1999-03-23
/ NUMBER OF SEQ ID NOS: 121
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 61
/ LENGTH: 1046
/ TYPE: DNA
/ ORGANISM: Arabidopsis thaliana
/ FEATURE:
/ OTHER INFORMATION: G233
US-09-533-029-61
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Query Match      16.1%; Score 193.6; DB 3; Length 1046;
Best Local Similarity 71.9%; Pred. No. 1.5e-31;
Matches 253; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 79 ATGGGAGGAGCTCCGCTGCTGCGAGAGATGGGCTCAAGAAAGGCTCATGAGCGCCGAG 138
DB 46 ATGGGAGAGCTCCATCTGCTGAGAGATGGGCTTGAAGAGAGACATGACACTGAA 105
QY 139 GAGGACAAAGTCTCTGCTGCGCCACATCCAGCGCCAGCGCAACTGGCGGCGCTTG 198
DB 106 GAAGATCAATCTTGCTCTCTTTATCTTCACATGACATGATGTAATCTGGCGAGCCCTC 165
QY 199 CCCAGCAAGCCGGGCTGCTGCTGCGGCAAGAGCTGCCGGTCCGGTGGATCATCTAC 258
DB 166 CCTAAGCAAGCTGCTGCTTTTGAATGTGAAAAAGCTGTAGACTTGGATGAACCTAT 225
QY 259 CTGGGCGGACATCAAGCGGGGCACTTCTCCAGAGAGAGAGACATCATCTCAT 318
DB 226 TTAAGCTGATATTAAAGCTGCAATTCACCAAGAGAGAAAGATGCTATCATCAGC 285
QY 319 CTCACGAGCTGTTGGCAACAGGTGTCGCAATTGCCGCAAGTTGCCCGGAGAGAGC 378
DB 286 TTACACCAATACTTGGCAATAGATGTGAGCATTCGAGCAAACTGCCTGGAGAACCC 345
QY 379 GACCAAGATCAAGAACTGTGGCACACCCCACTCAAGAAAGGCTTCGATG 430
DB 346 GATTAAGATCAAGAACTGTGGCACACCTCAAGAAAGAGACTCGAAG 397
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RESULT 5
US-09-640-211A-1965
/ Sequence 1965, Application US/09640211A
/ Patent No. 6833446
/ GENERAL INFORMATION:
/ APPLICANT: Wood, Marion
/ APPLICANT: Shenk, Michael A.
/ APPLICANT: McGrath, Annette
/ APPLICANT: Glenn, Matthew
/ TITLE OF INVENTION: Compositions and Methods for the
/ FILE REFERENCE: 11000.1021CIU
/ CURRENT APPLICATION NUMBER: US/09/640,211A
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/ CURRENT FILING DATE: 2000-08-16
/ NUMBER OF SEQ ID NOS: 2368
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1965
/ LENGTH: 424
/ TYPE: DNA
/ ORGANISM: Eucalyptus grandis
US-09-640-211A-1965
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Query Match      16.1%; Score 193.4; DB 3; Length 424;
Best Local Similarity 69.4%; Pred. No. 1.3e-31;
Matches 263; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

QY 58 ACAGGGAAGAGCAACACATATGGGAGAGGCTCCGCTGCGAGAAATGGGGCTCAAG 117
DB 25 AGCGGAGGAGGAGGAGAGAGATGGGAGAGCGAGCCGCTGCTGCGACAAAGCTTGGGAGAG 84
QY 118 AAGGTCATGAGACGCGGAGAGAGCAAGTCTTCTGCGCCACATCCAGCGCCAGCGC 177
DB 85 AAAGGCGCTGAGACGCGGAGAGAGCAAGAGCTGTCACTTCACTACCCAGCGC 144
QY 178 CACGCACTGGGCGGCTGCGCCAAAGCAAGCGGCTGCTGCTGCGGCAAGAGCTGC 237
DB 145 CATGCTGCTGGCGGCGCGCTCCCAAGCTCGCTGGGCTCGCGCTGTGGAAGAGCTGC 204
QY 238 CGCTCCGCTGATCAACTACTGCGCGCGGACATCAAGCGGCGCAACTTCTCAAGAG 297
DB 205 CGCTCCGCTGAGCAACTACTGCGCGCGGATCTCAAGCTGCGCTCAATGAGAGCC 264
QY 298 GAGGAGACACCATCATCTCCAGAGCTGCTTGGCAAGAGTGTGCGCAATTTGCC 357
DB 265 GAGGAAAGCTGCTTATCATCTCCATGCACTTCCGCAATAGGTGTCCAAATAGCA 324
QY 358 GCCAGTTGCCGCGGAGAGAGCAAGATCAAGAGTGTGCGCAACCACTCAAG 417
DB 325 GCTAGACTACCGGAAAGAGCAAGATCAAAAACTAGTGAACCATATCAAG 384
QY 418 AAGCGCTGATGCGCCGG 436
DB 385 AAGAGCTCATTAAGATGG 403
```

```
RESULT 6
US-09-640-211A-252
/ Sequence 252, Application US/09640211A
/ Patent No. 6833446
/ GENERAL INFORMATION:
/ APPLICANT: Wood, Marion
/ APPLICANT: Shenk, Michael A.
/ APPLICANT: McGrath, Annette
/ APPLICANT: Glenn, Matthew
/ TITLE OF INVENTION: Compositions and Methods for the
/ FILE REFERENCE: 11000.1021CIU
/ CURRENT APPLICATION NUMBER: US/09/640,211A
/ NUMBER OF SEQ ID NOS: 2368
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 252
/ LENGTH: 563
/ TYPE: DNA
/ ORGANISM: Eucalyptus grandis
US-09-640-211A-252

Query Match      16.0%; Score 192.6; DB 3; Length 563;
Best Local Similarity 72.5%; Pred. No. 2.1e-31;
Matches 263; Conservative 0; Mismatches 99; Indels 1; Gaps 1;

QY 55 CAGAGGAGGAAAGAGCAACATATGGGAGAGGCTCCGCTGCGAGAAAGATGGGCTC 114
DB 193 CAGAGGCTGCGCGCGAGAGACATGAGATCCCTTGTGCGAGAAAGCGCACACC 252
QY 115 AAGAAAGTTCATGACGCGGAGAGAGCAAGTCTCTGCTGCGCCACATCCAGCGCAC 174
```


US-09-640-211A-1718

Query Match 15.6%; Score 188; DB 3; Length 631;
Best Local Similarity 72.1%; Pred. No. 2e-30;
Matches 245; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

QY 79 ATGGGAGGAGCTCCGCTGTCGAGAAAGTGGGCTCAAGAGGGCTCATGAGCGCGGAG 138
DB 107 ATGGGAGAGATCTCTGCTGTGTAAGAAAGCTCATACAAACAAAGGGCGTGGACCAAGAA 166
QY 139 GAGGACAGAGTCTCTGCTGCGCCATCCAGCGCCAGCGCCAGCAATGGCGCGCTG 198
DB 167 GAGGAGAGATGCTCTATCCGCCCATCTCGAACTCAGGGGAGAGTGGCGGCTGCTT 226
QY 199 CCCAAGCAAGCCGGGCTGCTGCTTGGCGCAAGAGTCCGGGCTCCGGTGGATCAACTAC 258
DB 227 CCCAAGCGCGCAGGGGCTGATGCGCTCGGGAGAGAGCTGCGAGCTCCGATGATMAACTAC 286
QY 259 CTGCGGCGGAGATCAAGGGGGGCACTTCTCCAGAGGAGGAGACCATCATCCAT 318
DB 287 CTGCGTCTGATCTGAAGCGTGAAGAACTTCTCAGAAAGAGAGACGAACTGTCATCAA 346
QY 319 CTCACAGAGTCTGCTGCGCAACAGTGTGTCGCAATTGCCGCGAGTTGCCGGGAGAGAG 378
DB 347 CTCCACTCCCTACTCGGCAACAGTGTGTCTTATTGCAAGGAGATTTGCCGGGAGAG 406
QY 379 GACACGAGATCAAGAACTGTGGCAACCCACCTCAAG 418
DB 407 GACACGAGATMAAGAACTAGTGAATACATCATCAAG 446

RESULT 10

US-09-640-211A-2088
; Sequence 2088, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1021CIU
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2088
; LENGTH: 1150
; TYPE: DNA
; ORGANISM: Pinus radiata
US-09-640-211A-2088

Query Match 15.6%; Score 188; DB 3; Length 1150;
Best Local Similarity 72.1%; Pred. No. 2e-30;
Matches 245; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

QY 79 ATGGGAGGAGCTCCGCTGTCGAGAAAGTGGGCTCAAGAGGGCTCATGAGCGCGGAG 138
DB 63 ATGGGAGAGATCTCTGCTGTGTAAGAAAGCTCATACAAACAAAGGGCGTGGACCAAGAA 122
QY 139 GAGGACAGAGTCTCTGCTGCGCCATCCAGCGCCAGCGCCAGCAATGGCGCGCTG 198
DB 123 GAGGAGAGATGCTCTATCCGCCCATCTCGAACTCAGGGGAGAGTGGCGGCTGCTT 182
QY 199 CCCAAGCAAGCCGGGCTGCTGCTTGGCGCAAGAGTCCGGGCTCCGGTGGATCAACTAC 258
DB 183 CCCAAGCGCGCAGGGGCTGATGCGCTCGGGAAGAGCTGCAAGGCTCGATGATMAACTAC 242
QY 259 CTGCGGCGGAGATCAAGGGGGCACTTCTCCAGAGGAGGAGACCATCATCCAT 318
DB 243 CTGCGTCTGATCTGAAGCGTGAAGAACTTCTCAGAAAGAGAGACCACTCGTCATCAAA 302

QY 319 CTCACAGAGTCTGCTGCGCAACAGTGTGTCGCAATTGCCGCGAGTTGCCGGGAGAGAG 378
DB 303 CTCCACTCCCTACTCGGCAACAGTGTGTCTTATTGCAAGGAGATTTGCCGGGAGAG 362
QY 379 GACACGAGATCAAGAACTGTGGCAACACCACCTCAAG 418
DB 363 GACACGAGATMAAGAACTAGTGAATACATCATCAAG 402

RESULT 11

US-09-640-211A-2087
; Sequence 2087, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1021CIU
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2087
; LENGTH: 473
; TYPE: DNA
; ORGANISM: Pinus radiata
US-09-640-211A-2087

Query Match 15.1%; Score 181.6; DB 3; Length 473;
Best Local Similarity 70.9%; Pred. No. 4.2e-29;
Matches 241; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 79 ATGGGAGGAGCTCCGCTGTCGAGAAAGTGGGCTCAAGAGGGCTCATGAGCGCGGAG 138
DB 40 ATGGGAGAGATCTCTGCTGTGTAAGAAAGCTCATACAAAGGGCGTGGACTAAGAA 99
QY 139 GAGGACAGAGTCTCTGCTGCGCCATCCAGCGCCAGCGCCAGCAATGGCGCGCTG 198
DB 100 GAAAGACAGCCGCTTATCCCTCACTCAGAGCCAGCGGAGAGGGGCTGCGTGTG 159
QY 199 CCCAAGCAAGCCGGGCTGCTGCTTGGCGCAAGAGTGTCCGGTCCGGTGGATCAACTAC 258
DB 160 CCCAAGCGCGCAGGGGCTGCTGAGATGCGGCAAGAGCTGCAAGCTGATGATMAACTAC 219
QY 259 CTGCGGCGGAGATCAAGCGGGCACTTCTCCAGAGGAGGAGACCATCATCCAT 318
DB 220 CTGCGTCCGATCTGAAGGCTGGAAGCTTACCGAAGAGAGAGAGCTCATCACTAA 279
QY 319 CTCACAGAGTCTGCTGCGCAACAGTGTGTCGCAATTGCCGCAAGTTGCCCGAGGAGAGAG 378
DB 280 CTCCACTCCCTGCTTGGCAAGAGTGTCTTAAATTGCAAGGAGATTTGCCGGACGAGAG 339
QY 379 GACACGAGATCAAGAACTGTGGCAACCCACCTCAAG 418
DB 340 GACACGAGATMAAGAACTAGTGAACACACATCAAGAA 379

RESULT 12

US-09-640-211A-2105
; Sequence 2105, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1021CIU
; CURRENT APPLICATION NUMBER: US/09/640,211A

CURRENT FILING DATE: 2000-08-16

NUMBER OF SEQ ID NOS: 2368

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 2105

LENGTH: 1576

TYPE: DNA

ORGANISM: Pinus radiata

US-09-640-211A-2105

Query Match

Best Local Similarity 15.1%; Score 181.6; DB 3; Length 1576;

Matches 241; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 79 ATGGGAGGCGTCCGCTGCTGCGAAGATGGGGCTCAAGAGGCTTCATGAGCGCGGAG 138

DB 40 ATGGGAGATCTCCGCTGCTGTAAGGCTCATACTATAAGAGGCGCTGTAACAA 99

QY 139 GAGACAAAGTCTCTGCTCCCAATCAGCGCCAGCGCACTGCGCGCGCTG 198

DB 100 GAAGACGACCGCTTATCCCTCAGATTGAGCCAGCGGAGGGGCTGGCGTTGCTT 159

QY 199 CCCAAGCAAGCGGGCTGCTGCTGCGCAAGAGTCCCGGCTCCGTTGATCAATAC 258

DB 160 CCCAAGCGCGGCTGCTGAGATCGGCAAGAGCTGCACTGCGATGATTAACATAC 219

QY 259 CTGGCGCGGACATCAAGGGGGCACTTCTCCAGAGAGAGGACCATCATTCAT 318

DB 220 CTGGCGCTCCGATCTGAAGGTGAAGCTTCCAGAAAGAAAGACAGCTCATCATCA 279

QY 319 CTCACGAGCTGCTTGGCAACAGTGTCCGCAATTCGCCAGGTTGCCCGGAGAGAG 378

DB 280 CTCACCTCTGCTTGGCAACAGTGTCTTTAATTGAGGAGATGTCGCGAGCGAGC 339

QY 379 GACACGAGATCAAGACGTGTGGCAACCCACCTTAAGA 418

DB 340 GACACGAGATTAAGAACTACTGGAACACACATCAAAA 379

QY 379 GACACGAGATCAAGACGTGTGGCAACCCACCTTAAGA 418
DB 340 GACACGAGATTAAGAACTACTGGAACACACATCAAAA 379

RESULT 13

US-09-640-211A-2075

Sequence 2075; Application US/09640211A

Patent No. 6833446

GENERAL INFORMATION:

APPLICANT: Wood, Marion

APPLICANT: Shenk, Michael A.

APPLICANT: McGrath, Annette

TITLE OF INVENTION: Compositions and Methods for the

FILE REFERENCE: 11000.1021CIU

CURRENT FILING DATE: 2000-08-16

NUMBER OF SEQ ID NOS: 2368

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 2075

LENGTH: 636

TYPE: DNA

ORGANISM: Eucalyptus grandis

US-09-640-211A-2075

Query Match

Best Local Similarity 15.1%; Score 181.2; DB 3; Length 636;

Matches 246; Conservative 0; Mismatches 108; Indels 0; Gaps 0;

QY 73 AGCACATGGGAGGCTCTCGTCCGCAATCCAGCGCGCGCAACTGGAGC 132

DB 61 AGCACAGACCGCAACGCGCATGTGCAAGAGTGGGATTAAGAGAGCCCGTGGAGC 120

QY 133 CCGAGGAGAGCAAGGCTCTCGTCCGCAATCCAGCGCGCGCAACTGGAGC 192

DB 121 CCGAGGAGAGCAAGGCTCTCGTCCGCAATCCAGCGCGCGCAACTGGAGC 180

QY 193 GCCCTGCCAAGCAAGCGGCTGCTGCTTGGCGGCAAGCTGCCGCTCCGTTGATC 252

DB 181 ACCCTCCGAGACGCTGCTGCTCCAGCGCTGCGGCAAGAGCTGCCCTCGCTGATG 240

QY 253 AACTACTGCGCGCGGACATCAAGCGGGCAACTTCTCCAGAGAGAGAGACCATC 312

DB 241 AACTACTGCGCGCGCTCGCTCAAGAGAGCGGATGCTCCCGATGAGAGAGCTCATC 300

QY 313 ATCCATCTCCAGAGCTGTTGGCAACAGTGTGTCGCAATTGGCCGCAAGTTGGCCGGG 372

DB 301 CTCGCCCTCCAGCGCTCTTGGAAACAGTGTCTTTGATAGCTGGAAGAAATCCGGGC 360

QY 373 AGGAGGACCAAGAGATCAAGAACGTGTGGCACACCCACTTCAGAGGCGCTC 426

DB 361 CGCACGCAACGAGATCAAGAACTACTGGAACACCCACTCAGCAAAAAGCTC 414

QY 373 AGGAGGACCAAGAGATCAAGAACGTGTGGCACACCCACTTCAGAGGCGCTC 426

DB 361 CGCACGCAACGAGATCAAGAACTACTGGAACACCCACTCAGCAAAAAGCTC 414

RESULT 14

US-09-640-211A-1797

Sequence 1797; Application US/09640211A

Patent No. 6833446

GENERAL INFORMATION:

APPLICANT: Wood, Marion

APPLICANT: Shenk, Michael A.

APPLICANT: McGrath, Annette

APPLICANT: Glenn, Matthew

TITLE OF INVENTION: Compositions and Methods for the

FILE REFERENCE: 11000.1021CIU

CURRENT FILING DATE: 2000-08-16

NUMBER OF SEQ ID NOS: 2368

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1797

LENGTH: 509

TYPE: DNA

ORGANISM: Pinus radiata

US-09-640-211A-1797

Query Match

Best Local Similarity 15.0%; Score 180; DB 3; Length 509;

Matches 240; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

QY 79 ATGGGAGGAGCTCTGCTGCGAAGATGGGGCTCAAGAGGCTCAATGAGCGCGAG 138

DB 45 ATGGGAGATCTCCGCTGCTGTAAGAGCTCATTAACAAAGGGCGCTGATTAACAA 104

QY 139 GAGGACAAAGTCTGCTGCCCAATCCAGCGCGCGCAACTGGCGCGCTG 198

DB 105 GAAGATGACCGCTTATGCTCACAATCGAGCCACGCGGAAGGGGCTGGTCTCTT 164

QY 199 CCCAAGCAAGCGGCTGCTGCTGCGGCAAGAGCTGCCGCTCCGGTGAATCAACTAC 258

DB 165 CCCAAGCGCGGCTGCTGATGATGCGCAAGAGCTGCACTCGATGATTAACATAC 224

QY 259 CTGGCGCGGACATCAAGCGGGCAACTTCTCCAGAGAGAGAGACACATCATCAT 318

DB 225 CTGGCTCCGATCTGAAGGTGAAGCTTCAACGAAGAAAGAGAGAGCTCATCAAA 284

QY 319 CTCACGAGCTGCTTGGCAACAGTGTGTCGCAATTGGCCGCAAGTTGGCCGGAGAG 378

DB 285 CTCACCTCTGCTTGGCAACAGTGTGCTTTAATTGAGGAGATGTCGCGAGCGAGC 344

QY 379 GACACGAGATCAAGACGTGTGGCACACCCACTCAAGA 418

DB 345 GACACGAGATTAAGAACTACTGGAACACACATCAAAA 384

RESULT 15

US-09-640-211A-1982

Sequence 1982; Application US/09640211A

Patent No. 6833446

GENERAL INFORMATION:

APPLICANT: Wood, Marion


```

? APPLICANT: Sheink, Michael A.
? APPLICANT: McGrath, Annette
? APPLICANT: Glenn, Matthew
? TITLE OF INVENTION: Compositions and Methods for the
? TITLE OF INVENTION: Modification of Gene Transcription
? FILE REFERENCE: 11000.1024C10
? CURRENT APPLICATION NUMBER: US/09/640,211A
? CURRENT FILING DATE: 2000-08-16
? NUMBER OF SEQ ID NOS: 2368
? SOFTWARE: FASTSEQ for Windows Version 4.0
? SEQ ID NO 1982
? LENGTH: 373
? TYPE: DNA
? ORGANISM: Plinus radiata
US-09-640-211A-1982

```

Query Match	14.9%	Score 179;	DB 3;	Length 373;
Best Local Similarity	72.1%	Pred. No. 1.4e-28;		
Matches 233;	Conservative	0;	Mismatches 90;	Indels 0;
			Gaps	0;

Oy	79	ATGGGAGGGCTTC	CGGTGCGAGAAAGATGGGCTCAAGAAAGGCTCATGTGACGGCGAG	138
Db	51	ATGGGAGATCTTC	CTCTGTGAAAAGCTCATACAAACAAAGGGCGTGGACCAAGA	110
Oy	139	GAGACAAAGTCTCT	CGCCCATCATCCAGCCCATCGGCCACGGCACTGGCGGCTG	198
Db	111	GAGACGATCGCTCT	ATGCCCATTTCCAACTCAAGGGGAAAGTTGCTGGCCCTGCTT	170
Oy	199	CCCAAGCAAGCGGG	CTGCTGCGGCAAGAGCTGCGGCTCCGGTGGATCAACTAC	258
Db	171	CCCAAGGCGCGAG	GGCTGATGCGGGAAGAGCTGCAGGCTCCGATGGATTAAGCTAC	230
Oy	259	CTGCGGCGGACAT	CAAGCTGGGGCACTTCTCCAAGAGAGGAGGACACCATATCCAT	318
Db	231	CTGCTCTCTGATCT	GAGCGTGGAACTTCTCAAGAAAGAAACAACATCATATCAAA	290
Oy	319	CTCCAGAGCTGCTT	GGCAACAGTGGTCCGCATATGCGCGCAGTTGCCGGGAGGACG	378
Db	291	CTCCACTCCCTACT	CGGGCAACAAGTGGTCTCTTATTGACAGCGAGATTGGCGGGGACG	350
Oy	379	GACCAACGAGATCA	AGAACGTGTG	401
Db	351	GACCAACGAGATTA	AGAACTACTG	373

Search completed: June 24, 2006, 19:41:23
Job time : 467 secs

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OM nucleic - nucleic search, using sw model

Run on: June 25, 2006, 07:59:45 ; Search time 5480 Seconds
(without alignments)
1265.518 Million cell updates/sec

Title: US-10-521-811-1

Perfect score: 1202

Sequence: 1 cagccgcctccctcccaaga.....gctaaaaaaaaaaaaaaa 1202

Scoring table: IDENTITY_NUC

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Searched: 48236798 seqs, 2795965780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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12: gb_esc13:*
13: gb_esc14:*
14: gb_esc15:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	774	64.4	774	13	CL969261 AB118162
2	635	52.8	638	1	AB118162
3	608.4	50.6	621	5	CK008102 27953781c
4	586.2	48.8	601	5	CF986244 15532781c
5	583	48.5	594	5	CK014002 32319781c
6	581.6	48.4	657	2	BI805305 S035C08 S
7	577	48.0	585	5	CK014563 32790781c
8	567.4	47.2	581	5	CK011009 29726781c
9	548.4	45.6	550	5	CI166609 2166609
10	546	45.4	561	5	CF990405 24029781c
11	532	44.3	550	5	CI261029 10191781c
12	530.2	44.1	545	5	CF986458 10191781c
13	523.6	43.6	544	5	CF988227 17600781c
14	497	41.3	509	5	CK008265 33406781c
15	493	41.0	500	5	CI175768 2175768
16	487.4	40.5	500	5	CI163884 2163884
17	475	39.5	500	5	CI167187 2167187
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25	407.8	33.9	1123	10	DR738936
26	395.6	32.9	460	4	C72644
27	391	32.5	410	3	BP432988
28	385.8	32.1	432	2	BM421359
29	376.2	31.3	847	10	DR814848
30	368.2	30.6	834	10	DR804074
31	351.4	29.2	453	2	BM420650
32	351	29.2	874	10	DV472233
33	350.4	29.2	824	10	DV473866
34	350	29.1	893	10	DR741522
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36	340.2	28.3	1082	10	DR741556
37	339.6	28.3	673	3	BQ837968
38	335	27.9	777	7	BF617565
39	331.6	27.6	681	3	BO763917
40	331	27.5	784	10	DV174489
41	330.2	27.5	840	10	DV858941
42	327.8	27.3	1075	10	DR741858
43	327.4	27.2	329	4	CB000724
44	327.4	27.2	609	2	BG300704
45	327.4	27.2	935	2	BG343209

ALIGNMENTS

RESULT 1
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LOCUS CL969261 774 bp DNA linear GSS 21-SEP-2004
DEFINITION OSIFCC018187 Oryza sativa Expressed library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.
ACCESSION CL969261
VERSION CL969261.1 GI:52393152

SOURCE

ORGANISM Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BOP clade; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 774)

REFERENCE

Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M., Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L., Wong, G. K. S., Deng, X. W. and Wang, J.

An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis

Unpublished (2004)

JOURNAL

Comment: Chen Chen
Department of Bioinformatics
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559

Fax: 86-10-8048676

Email: chenchen@genomics.org.cn

Rice genomic sequence.

Class: exon-trapped.

Location/Qualifiers

FEATURES

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QY	139	GAGGCAAGAGTCTTGTCGCGCCCAATCCAGCGCCAAGGCGCAACGCGCAACTGCGCGCCCTG	198
Db	61	GAGGCAAGAGTCTTGTCGCGCCCAATCCAGCGCCCAAGGCGCAACGCGCAACTGCGCGCCCTG	120
QY	139	CCCAAGCAAGCCGGGCTGCTGCTGGGGCAAGAGCTGCGGGCTCCGGTGGGATCAACTAC	258
Db	121	CCCAAGCAAGCCGGGCTGCTGCTGGGGCAAGAGCTGCGGGCTCCGGTGGGATCAACTAC	180
QY	259	CTGCGGCGCGGACATTCAGCGGGGCAACTTCTTCCAGAGAGAGAGACCAACCATCATCAT	318
Db	181	CTGCGGCGCGGACATTCAGCGGGGCAACTTCTTCCAGAGAGAGAGACCAACCATCATCAT	240
QY	319	CTCCACGAGCTGCTTGGGCAACAGTGTGTGTCGCAATTGCGCGCAGTGTGCCGGGAGAGC	378
Db	241	CTCCACGAGCTGCTTGGGCAACAGTGTGTGTCGCAATTGCGCGCAGTGTGCCGGGAGAGC	300
QY	379	GACAAACGAGATTCAGAAAGCTGTGGGCAACCCACCTCAAGAGAGCGCTTCGATCGCGCT	438
Db	301	GACAAACGAGATTCAGAAAGCTGTGTGGCAACCCACCTCAAGAGAGCGCTTCGATCGCGCT	360
QY	439	CAGGCGGTCATGTGCGCGGCAAGCGCGGCAAGAAACAAGAGAGCCGAGAGCGCGAG	498
Db	361	CAGGCGGTCATGTGCGCGGCAAGCGCGGCAAGAAACAAGAGAGCCGAGAGCGCGAG	420
QY	499	AAGCCAGCG	558
Db	421	AAGCCAGCG	480
QY	559	GTGACGAGTCTTCGATGAGCCTTCGTGCGTGGCGAGAGACACGCGCAACGCGCGGATCAGC	618
Db	481	GTGACGAGTCTTCGATGAGCCTTCGTGCGTGGCGAGAGACACGCGCAACGCGCGGATCAGC	540
QY	619	TGCGGTCGCGCTCCGTCGTGGCGCAAGAGAGAGAGTCTTCACTCGGCTTCCGAGGAG	678
Db	541	TGCGGTCGCGCTCCGTCGTGGCGCAAGAGAGAGAGTCTTCACTCGGCTTCCGAGGAG	600
QY	679	TTCCAGATTCGACGAGCCTTCGTGTCGAGAGACGCTGTGATGCGCTGGAAGGATACAC	738
Db	601	TTCCAGATTCGACGAGCCTTCGTGTCGAGAGACGCTGTGATGCGCTGGAAGGATACAC	660
QY	739	GTGTCCATGAGACCCCGGAGACGCGCTTTCGTGCGCGCCCATTCGCGCAGACATGAGCTAC	798
Db	661	GTGTCCATGAGACCCCGGAGACGCGCTTTCGTGCGCGCCCATTCGCGCAGACATGAGCTAC	720
QY	799	TGGCTCGGAGTGTTCATGATGAGTCCGGCAAGGCGCAAGACTTGGCGCAGATCTAG	852
Db	721	TGGCTCGGAGTGTTCATGATGAGTCCGGCAAGGCGCAAGACTTGGCGCAGATCTAG	774
RESULT 2			
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DEFINITION	AB118162 ZAP1 rice Oc cDNA Oryza sativa (indica cultivar-group)		
ACCESSION	AB118162		
VERSION	AB118162.1	GI:45244940	
KEYWORDS	EST.		
SOURCE	Oryza sativa (indica cultivar-group)		
ORGANISM	Oryza sativa (indica cultivar-group)		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.		
AUTHORS	1 (baees 1 to 638)		
TITLE	Fujiwara, S., Tanaka, N., Kaneda, T., Takayama, S., Che, F. and Isozaki, A.		
JOURNAL	Analysis of flagellin perception signaling and role of flagellin in rice immune system using cDNA microarray		
COMMENT	Unpublished (2004)		
	Contact: Fang-Sik Che		

Graduate School of Biological Sciences
Nara Institute of Science and Technology
816-5, Ikoma-shi, Takayama-chou, Nara 630-0101, Japan
Tel.: 81-743-72-5452
Fax: 81-743-72-5459
Email: tschoban.alist-nara.ac.jp, URL: <http://bwsj.alist-nara.ac.jp>
Location/Qualities

FEATURES	Location/Qualifiers
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Db	64	AGGAAAGAGCAACACAAATGGGGAGGGCTCCGTCTGCGAAGATGGGGCTCAAGAG	123
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Db	124	GGTCCATGAGAGCGCGAGAGAGAACAAAGTCTCTGTCGCCCATCTCAACGGCCAC	183
OY	181	GGCAACTGCGCGCGCTCCGCCCAAGACCGGGCTGCGCTTGGCGAGAGCTGCCG	240
Db	184	GGCAACTGCGCGCGCTCCGCCCAAGACCGGGCTGCGCTTGGCGAGAGCTGCCG	243
OY	241	CTCCGGTGAGTCAACTACTGCGCGCGCATCAAGCGGGCCACTTCTTCAAGAGAG	300
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Db	424	CGCTTCGATGCGCGGCTCAGGGCGGTCATGTCCGCGAAGCGCGGCAAGAGACAAG	483
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Db	484	AAGCCGAAGACGCGAAGAACCAACGCGCGCGCGCGCGCGCGCGCGCGCTGCCCGAG	543
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Db	544	CGGTCCGCTCTGTGTCGTGAGCGAAGTCTTCGATGCTTGTGCTGGCGAGAGACAC	603
OY	601	GGCAACGCGGGATCAGCTCGGCGCTCGCGCTCGG	635
Db	604	GGCAACGCGGGATCAGCTCGGCGCTCGCGCTCGG	638

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CK008102			EST 04-FEB-2005

DEFINITION 27953rslcfe4052.y1 Oryza sativa cv. PA64s panicle sterile cDNA
Library Oryza sativa (indica cultivar-group) cDNA 5', mRNA
sequence.
ACCESSION CK008102
VERSION CK008102.1 GI:58597574
KEYWORDS EST.
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 621)
AUTHORS Yu, J., Wang, J., Lin, W., Li, S., Li, H., Zhou, J., Ni, P., Dong, W.,
Hu, S., Zeng, C., Zhang, J., Zhang, Y., Li, R., Xu, Z., Li, S., Li, X.,
Zheng, H., Gong, L., Lin, L., Yin, J., Geng, J., Li, G., Shi, J., Liu, J.,
Lv, H., Li, J., Wang, J., Deng, Y., Ran, L., Shi, X., Wang, X., Wu, Q.,
Li, C., Ren, X., Wang, J., Wang, X., Li, D., Liu, D., Zhang, X., Ji, Z.,
Zhao, W., Sun, Y., Zhang, Z., Bao, J., Han, Y., Dong, L., Ji, J., Chen, P.,
Wu, S. and Liu, J.
TITLE The Genomes of Oryza sativa: A History of Duplications
JOURNAL PLOS Biol. 3 (2), e38 (2005)
PUBMED 15685292
COMMENT Contact: Yan Zhou
Bioinformatics Department
Hangzhou Genomics Institute
No.51 Zhijiang Road, Hangzhou 310008, China
Tel: 86-571-56805886
Fax: 86-571-56805884
Email: zhouyan@genomics.org.cn
Seq primer: M13 Forward
High quality sequence stop: 621
POLYA-No.
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library"
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Db 12 CGGCGTCCGCGGAGCGGCTCGCTCGTGGTGAAGAGTCTCGATGGCTCTCGG 71
Oy 587 TGGCGGAGAGGACGCGCAAGCGCGGATCAGCTCGGCGTCCGCGTCCGTCGCGCAAG 646
Db 72 TGGCGGAGAGGACGCGCAAGCGCGGATCAGCTCGGCGTCCGCGTCCGTCGCGCAAG 131
Oy 647 AGGAGAGCTCTTCACTTCGCGCTTCGAGAGGTTCCAGATCGACGACGCTTGTGCG 706
Db 132 AGGAGAGCTCTTCACTTCGCGCTTCGAGAGGTTCCAGATCGACGACGCTTGTGCG 191
Oy 707 AGAGCTGTGCAGTCCGCTGGAAGCGGTTAGAGCTGTGCATGAGCCCGCGGAGCGCTTG 766
Db 192 AGAGCTGTGCAGTCCGCTGGAAGCGGTTAGAGCTGTGCATGAGCCCGCGGAGCGCTTG 251
Oy 767 TGGCGCGCGCATCCGCGGAGCATGAGTACTGCTCGAGTGTTCATGAGTCCGCGG 826
Db 253 TGGCGCGCGCATCCGCGGAGCATGAGTACTGCTCGAGTGTTCATGAGTCCGCGG 311
Oy 827 AAGCGCAGACTTCCGCGGAGTCTAGAGAAAGAGAGAAATTTTACGTTTCTCGGTTA 886
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LOCUS CF986244
DEFINITION 15532rslcfe41417.y1 Oryza sativa cv. LYP9 tillering whole plant
cDNA library Oryza sativa (indica cultivar-group) cDNA 5', mRNA
sequence.
ACCESSION CF986244 GI:58587936
VERSION CF986244
KEYWORDS EST.
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 601)
AUTHORS Yu, J., Wang, J., Lin, W., Li, S., Li, H., Zhou, J., Ni, P., Dong, W.,
Hu, S., Zeng, C., Zhang, J., Zhang, Y., Li, R., Xu, Z., Li, S., Li, X.,
Zheng, H., Gong, L., Lin, L., Yin, J., Geng, J., Li, G., Shi, J., Liu, J.,
Lv, H., Li, J., Wang, J., Deng, Y., Ran, L., Shi, X., Wang, X., Wu, Q.,
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Zhao, W., Sun, Y., Zhang, Z., Bao, J., Han, Y., Dong, L., Ji, J., Chen, P.,
Wu, S. and Liu, J.
TITLE The Genomes of Oryza sativa: A History of Duplications
JOURNAL PLOS Biol. 3 (2), e38 (2005)
PUBMED 15685292
COMMENT Contact: Yan Zhou
Bioinformatics Department
Hangzhou Genomics Institute
No.51 Zhijiang Road, Hangzhou 310008, China
Tel: 86-571-56805886
Fax: 86-571-56805884
Email: zhouyan@genomics.org.cn
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Matches 588; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 24 CACAACGCAAGAGAGACAGAGATTCAGATCAGAGCAGGAAAGAGCAAGCAATGGG 83

Db 11 CACAACGCAAGAGAGCAGACGATTCAATCAGACGAGGAAAGAGCAAGACAAAGGG 70
Oy 84 GAGGGCTCGTCTGCTGAGAGAGTGGGGCTCAAGAAAGGTCATGACGCCGAGAGAGA 143
Db 71 GAGGGCTCGTCTGCTGAGAGAGTGGGGCTCAAGAAAGGTCATGACGCCGAGAGAGA 130
Oy 144 CAAGGTCCTCGTCTGCTGAGAGAGTGGGGCTCAAGAAAGGTCATGACGCCGAGAGAGA 203
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Oy 384 CGAGATCAAGAAAGTGTGACACACCCCTCAAGAAAGCGCTGATGCGCGCTCAGGG 443
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Oy 504 AGCCG 563
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sequence.
ACCESSION CK014002
VERSION CK014002.1 GI:58603474
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SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BFP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 594)
Oy Yu.J., Wang,J., Lin,W., Li,S., Li,H., Zhou,J., Ni,P., Dong,W.,
Hu,S., Zeng,C., Zhang,J., Zhang,Y., Li,R., Xu,Z., Li,S., Li,X.,
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Zhao,W., Sun,Y., Zhang,Z., Bao,J., Han,Y., Dong,L., Ji,J., Chen,P.,
Wu,S. and Liu,J.
The Genomes of Oryza sativa: A History of Duplications
Plos Biol. 3 (2), e38 (2005)
15685292
COMMENT Contact: Yan Zhou
Bioinformatics Department
Hangzhou Genomics Institute
No.51 Zhijiang Road, Hangzhou 310008, China
Tel: 86-571-5680586
Fax: 86-571-56805884
Email: zhouyan@genomics.org.cn
Seq primer: M13 forward

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Oy 181 GGCACATGAGCGCCGAG 240
Db 192 GGCACATGAGCGCCGAG 251
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Db 492 AAGCGGAAGAGCGCAAG 551
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DEFINITION sativa cDNA clone 5035C08, mRNA sequence.
ACCESSION B1805305
VERSION B1805305.1 GI:15852509
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BFP
clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 657)
 AUTHORS Dong, H.T., Li, D.B., Zhuang, X.F., Dai, C.G., Sun, L.X., Pei, Y.X.,
 Wu, H.F., Jiang, Y.X., Yu, F.C., Gao, Q.K. and Lou, Y.C.
 TITLE A Gene Expression Screen in *Oryza sativa*
 JOURNAL Unpublished (2001)
 COMMENT Contact: Haitao Dong, Debao Li
 Bioinformatics and Gene Network Research Group
 Zhejiang University
 Kaixuan Road 268#, Hangzhou, Zhejiang, P.R.China
 Tel: 0086-571-86961525
 Fax: 0086-571-86961525
 Email: webmaster@estarray.org, URL: http://www.estarray.org
 Seq primer: M13 forward primer.

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 Matches 612; Conservative 0; Mismatches 14; Indels 2; Gaps 2;

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Oy 815 TGGAGTCCGCGGACCGCAAGATTGCGCGAGATCTAGAGAAAGAGAAATTTTACCG
Db 267 TGGAGTCCGCGGACCGCAAGATTGCGCGAGATCTAGAGAAAGAGAAATTTTACCG
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Db 327 TTTCTTGGTTAATTGATTTGTTTTTCTCTCTGCGCCATCTTTGACCGGAGGACA
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 library *Oryza sativa* (indica cultivar-group) cDNA 5', mRNA
 sequence.

ACCESSION CK014563
 VERSION CK014563.1 GI:58604035
 KEYWORDS EST.
 SOURCE *Oryza sativa* (indica cultivar-group)
 ORGANISM *Oryza sativa* (indica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BRP
 clade; Ehrhartoideae; Oryzaceae; *Oryza*.

REFERENCE

1 (bases 1 to 585)
 Yu, J., Wang, J., Lin, W., Li, S., Li, H., Zhou, J., Ni, P., Dong, W.,
 Hu, S., Zeng, C., Zhang, J., Zhang, Y., Li, R., Xu, Z., Li, S., Li, X.,
 Zheng, H., Cong, L., Lin, L., Yin, J., Geng, J., Li, G., Shi, J., Liu, J.,
 Lv, H., Li, J., Wang, J., Deng, Y., Ran, L., Shi, X., Wang, X., Wu, Q.,
 Li, C., Ren, X., Wang, J., Wang, X., Li, D., Liu, D., Zhang, X., Ji, Z.,
 Zhao, W., Sun, Y., Zhang, Z., Bao, J., Han, Y., Dong, L., Ji, J., Chen, P.,
 Wu, S. and Liu, J.

AUTHORS

TITLE The Genomes of *Oryza sativa*: A History of Duplications
 JOURNAL PLOS Biol. 3 (2), e38 (2005)
 PUBMED 15685292
 COMMENT Contact: Yan Zhou
 Bioinformatics Department
 Hangzhou Genomics Institute
 No. 51 Zhijiang Road, Hangzhou 310008, China
 Tel: 86-571-56805886
 Fax: 86-571-56805884
 Email: zhouyan@genomics.org.cn
 Seq primer: M13 Forward
 High quality sequence stop: 585
 POLYA=No.

FEATURES

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location/Qualifiers
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ORIGIN

Query Match 48.0%; Score 577; DB 5; Length 585;
 Best Local Similarity 100.0%; Pred. No. 7.9e-129;
 Matches 577; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	489	GAAGCGAACCCG	548
OY	558	GGTGACGAGTCTCTGATGGCTTCGTGGTGGCGGAG	594
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	library Oryza sativa (indica cultivar-group)		linear
	sequence.		EST 04-FEB-2005
			sterile cDNA
			CDNA 5', mRNA

ACCESSION	CK011009
VERSION	CK011009.1
KEYWORDS	GI:58600481
SOURCE	EST.
ORGANISM	<i>Oryza sativa</i> (indica cultivar-group)
	<i>Oryza sativa</i> (indica cultivar-group)

REFERENCE
YU, J., WANG, J., LIN, W., LI, S., LI, H., ZHOU, J., NI, P., DONG, W.,
1 (Bases 1 to 581)
clade, Erihartoideae; Oryzeae; Oryza.
Eukaryotes; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BPP
clade, Erihartoideae; Oryzeae; Oryza.

TITLE
JOURNAL
PUBMED

The Genomes of *Oryza sativa*: A History of Duplications
Plos Biol. 3 (2), e38 (2005)
15685292

COMMENT
Contact: Yan Zhou
Bioinformatics Department
Hangzhou Genomics Institute
No.51 Zhijiang Road, Hangzhou 310008, China
Tel.: 86-571-5660586
Fax: 86-571-56605884
Email: zhouyan@genomics.org.cn
Seq primer: MJ3 Forward
High quality sequence stop: 581
POLYA=No.

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molecule="mRNA"	
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dev_stage="heading/flowering"	
clone_lib="Oryza sativa cv. PA64s panicle sterile cdna library"	

ORIGIN				
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Best Local Similarity	99.7%	Pred. No. 1.7e-126		
Matches 579; Conservative	0	Mismatches 1	Indels 1	Gaps 1

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QY	80	TGGG-GAGGGCTCCGTGCTGGAGAAATGGGGCTCAAGAGGGTCCATGGA	138
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QY	139	GAGGACAAAGTCTCTGTGCCCCATCCAGCGCCACGGCACGGCACTGGCGGCTTG	198
Db	121	GAGGACAAAGTCTCTGTGCCCCATCCAGCGCCACGGCACCTGGCGGCTTG	180
QY	199	CCCAAGCAAGCCGGGCTGTGCTGGCGGCAAGACTCCGGCTCCGGTGAATCAACTAC	258
Db	181	CCCAAGCAAGCCGGGCTGTGCTGGCGGCAAGACTCCGGCTCCGGTGAATCAACTAC	240
QY	259	CTGCGGCGGCAATCAAGCGGGCAACTTCTCCAAAGAGAGAGAGACATCATCAT	318
Db	241	CTGCGGCGGCAATCAAGCGGGCAACTTCTCCAAAGAGAGAGAGACATCATCAT	300
QY	319	CTCCACGAGCTGCTTGGCAACAGGTGATCCGCATTGCGCCAGGTTGCCCGGAGAGAG	378
Db	301	CTCCACGAGCTGCTTGGCAACAGGTGATCCGCATTGCGCCAGGTTGCCCGGAGAGAG	360
QY	379	GACAAACGAGATCAAGAACGTGTGGCAACCCACTTCAAGAAAGCGCTCGATGCGCGCT	438
Db	361	GACAAACGAGATCAAGAAAGGTGTGGCAACCCACTTCAAGAAAGCGCTCGATGCGCGCT	420
QY	439	CAGGGCGGTCAATGTGCGGCGGCGGCGGCGGCAAGAGCACAAGAACCCGAAGAGCGGAG	498
Db	421	CAGGGCGGTCAATGTGCGGCGGCGGCGGCGGCAAGAGCAACAGAACCCGAAGAGCGGAG	480
QY	499	AAGCCAGCGCGCGCGCGCGCGCGCGCGCGCGCTGCCAGAGGGTCCGCTCTGTCTGG	558
Db	481	AAGCCAGCGCGCGCGCGCGCGCGCGCGCGCGCTGCCAGAGGGTCCGCTCTGTCTGG	540
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Db	541	GTGACGAGTCTTCGATGGCTCTGTGGTGGCGAGAGACA	581

RESULT 9	
C1166609	
LOCUS	
DEFINITION	
Oryza sativa (japonica cultivar-group) CDNA clone 031-M064R-D01 3'	
mRNA sequence.	
C1166609	550 bp
C1166609 Oryza sativa (japonica cultivar-group)	linear
Oryza sativa (japonica cultivar-group) shoot and callus	EST 06-FEB-2006

ACCESSION	C1166609	GI:86526403
VERSION	C1166609.1	
KEYWORDS	EST.	
SOURCE	Oryza sativa (japonica	
ORGANISM	Oryza sativa (japonica	

REFERENCE
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.

AUTHORS	Kikuchi, S.
TITLE	Collection and mapping of over 30,000 transcripition units by
JOURNAL	rice full-length cDNA project from japonica rice
COMMENT	Unpublished (2006)
	Contact: Shoshi Kikuchi

Department of Molecular Genetics, Head of Laboratory of Gene Expression
National Institute of Agrobiological Sciences
2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan
Tel: 81-29-838-7007
Fax: 81-29-838-7007
Email: skkuch@nias.affrc.go.jp
This EST clone is one of 780K ESTs of Rice full length cDNA Project
URL: <http://cna01.dna.affrc.go.jp/cDNA/>
NINS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K.,
Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yaezaki, J.,

Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Yamamoto, M., and Nakahama, Y.
FAIS Genome Sequencing & Analysis Group: Ootomo, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Mura, J., Mizuno, K., Naitaka, R., Nishikura, Y., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, J., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K., and Murakami, K.
Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carinici, P., Fukuda, S., Hanagami, T., Hara, A., Hoshizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murate, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Ootao, N., Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Saeki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takanashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A., and Hayashizaki, Y.

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Matches 549; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 121 CGAGCGGTGTCGCGCGCGCATCCGCGACGATGAGTACTGAGTGGAGTGTTCAT 180
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DB 481 GTGCAAACTGAGATCATCAGAAACGGGCTCTGCGTTTCATTTGATTAATTAATTCAA 540
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DB 541 CTTGCAAGCT 550

RESULT 10

LOCUS

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240295csee 5646.y1 Oryza sativa cv. LYP9 tillering whole plant
CDNA library Oryza sativa (indica cultivar-group) cDNA 5', mRNA
sequence.

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

1 (bases 1 to 561)
Yu, J., Wang, J., Lin, W., Li, S., Li, H., Zhou, J., Ni, P., Dong, W., Hu, S., Zeng, C., Zhang, J., Zhang, Y., Li, R., Xu, Z., Li, S., Li, X., Zheng, H., Cong, L., Lin, L., Yin, J., Geng, J., Li, G., Shi, J., Liu, J., Lv, H., Li, J., Wang, J., Deng, Y., Ran, L., Shi, X., Wang, X., Wu, O., Li, C., Ren, X., Wang, J., Wang, X., Li, D., Liu, D., Zhang, X., Ji, Z., Zhao, W., Sun, Y., Zhang, Z., Bao, J., Han, Y., Dong, L., Ji, J., Chen, P., Wu, S., and Liu, J.
The Genomes of Oryza sativa: A History of Duplications
Plos Biol. 3 (2), e38 (2005)
15685292
Contact: Yan Zhou
Bioinformatics Department
Hangzhou Genomics Institute
No. 51 Zhijiang Road, Hangzhou 310008, China
Tel: 86-571-56805886
Fax: 86-571-56805884
Email: zhouyan@genomics.org.cn
Seq primer: M13 Forward
High quality sequence stop: 561
POLYA=No.

FEATURES

source

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DB 16 CAGCGCCTCTCTTCCAGAACACACACGACGAGAGACGAGTTCAGATCAGAGC 75
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DB 76 AGGGAAGAGCAAGCAATGGGAGAGGCTCCGTGCTGGAGAAAGTGGGGCTCAAGAG 135
OY 121 GGTCAATGAGCGCGGAGAGAGCAAGAGTCTCTGCGCCACATCCAGGCCACGCGCAC 180
DB 136 GGTCAATGAGCGCGGAGAGAGCAAGAGTCTCTGCGCCACATCCAGGCCACGCGCAC 195
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Db 376 AGGTGTCGGGAG 435
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Db 496 AAGCCGAG 555
QY 541 GCGTCC 546
Db 556 GCGTCC 561

RESULT 11

C1261029

LOCUS C1261029 Oryza sativa (japonica cultivar-group) Shoot and root of
DEFINITION germinating seeds Oryza sativa (japonica cultivar-group) cDNA clone
C1261029
VERSION C1261029.1 GI:86854961

ACCESSION
KEYWORDS
SOURCE
ORGANISM

EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BBP
Clade; Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 550)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Collection and mapping of over 30,000 transcriptions units by the
rice full-length cDNA project from japonica rice
Unpublished (2005)
Contact: Shoshi Kikuchi
Department of Molecular Genetics, Head of Laboratory of Gene
Expression
National Institute of Agrobiological Sciences
2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan
Tel: 81-29-838-7007
Fax: 81-29-838-7007

Email: skikuchi@nias.affrc.go.jp
This EST clone is one of 780K ESTs of Rice full length cDNA Project
URL: <http://cdna01.dna.affrc.go.jp/cdna/>
NIAS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K.,
Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J.,
Ishikawa, M., Yamada, H., Ooka, H., Horita, I., Kojima, K., Naniwa, T.,
Ohneda, E., Yanagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T.,
Yamamoto, M., and Nakahama, Y.

FAIS Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y.,
Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M.,
Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Mura, J.,
Mizuno, K., Narikawa, R., Nikiura, J., Oka, M., Ryu, R., Sugano, S.,
Sugiyama, A., Suzukawa, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S.,
Yoshimura, A., Matubara, K., and Murakami, K.
Genome Exploration Research Group in Riken Genomic Sciences Center
and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K.,
Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T.,
Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K.,
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Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
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Saeki, D., Sato, K., Shibata, K., Shingawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F.,
Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K.,
Yasunishi, A., and Hayashizaki, Y.

FEATURES

SOURCE

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/clone="046-M008R-F02"
/cissue_type="Shoot and root of germinating seeds"
/clone_lib="Oryza sativa (japonica cultivar-group) Shoot
and root of germinating seeds"

ORIGIN

Query Match 44.3%; Score 532; DB 5; Length 550;
Best Local Similarity 99.8%; Pred. No. 6,5e-118;
Matches 543; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 634 GTGTGCGGCAAGAGAGAGAGCTCTTCACTTGGCTTCCAGAGAGCTTCCAGAGAGAG 693
Db 1 GTGTGCGGCAAGAGAGAGAGCTCTTCACTTGGCTTCCAGAGAGAGCTTCCAGAGAGAG 59

QY 694 AGCTTCTGTGGAG 753
Db 60 AGCTTCTGTGGAG 119

QY 754 GCGGAG 813
Db 120 GCGGAG 179

QY 814 ATGAGTCCGCGGAG 873
Db 180 ATGAGTCCGCGGAG 239

QY 874 GTTCTTGTGGTAAATGATTTGTTTCTCTCTCTGCGGAGAGAGAGAGAGAGAGAG 933
Db 240 GTTCTTGTGGTAAATGATTTGTTTCTCTCTCTGCGGAGAGAGAGAGAGAGAGAGAG 299

QY 994 ATAGCTAACAG 993
Db 300 ATAGCTAACAG 359

QY 994 CGATCGAGTGGAG 1053
Db 360 CGATCGAGTGGAG 419

QY 1054 CTTCCTGATGATGAG 1113
Db 420 CTTCCTGATGATGAG 479

QY 1114 ATGTCAAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1173
Db 480 ATGTCAAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 539

QY 1174 AACT 1177
Db 540 AACT 543

RESULT 12

CF966458/c

LOCUS CF966458 585 bp mRNA linear EST 15-JAN-2004
DEFINITION 10191xiced.10977.y1 Oryza sativa cv. LYP9 trefoil whole plant cDNA
library Oryza sativa (indica cultivar-group) cDNA 5', mRNA
sequence.

ACCESSION CF966458
VERSION CF966458.1 GI:38482419
KEYWORDS EST.

SOURCE	Oryza sativa (indica cultivar-group)
ORGANISM	Oryza sativa (indica cultivar-group)
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Euhartioideae; Oryzaceae; Oryza.
REFERENCE	1 (bases 1 to 585)
AUTHORS	Yu, J., Wang, J., Lin, W., Li, S., Li, H., Zhou, J., Ni, P., Dong, W., Hu, S., Zeng, C., Zhang, J., Zhang, Y., Li, R., Xu, Z., Li, S., Li, X., Zheng, H., Cong, L., Lin, L., Yin, J., Geng, J., Li, G., Shi, J., Liu, J., Lv, H., Li, J., Wang, J., Deng, Y., Ran, L., Shi, X., Wang, X., Wu, Q., Li, C., Ren, X., Wang, J., Wang, X., Li, D., Liu, D., Zhang, X., Ji, Z., Zhao, W., Sun, Y., Zhang, Z., Bao, J., Han, Y., Dong, L., Ji, J., Chen, P., Wu, S. and Liu, J.
TITLE	The Genomes of Oryza sativa: A History of Duplications
JOURNAL	PLoS Biol. 3 (2), e38 (2005)
PUBMED	15685292
COMMENT	Contact: Yan Zhou Bioinformatics Department Hangzhou Genomics Institute No.51 Zhijiang Road, Hangzhou 310008, China Tel: 86-571-56805886 Fax: 86-571-56805884 Email: zhouyan@genomics.org.cn Seq primer: M13 Forward High quality sequence scop: 585 POLYA=NO.
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Matches 543; Conservative	0; Mismatches 3; Indels 1; Gaps 1;
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QY	652 AGCTCTTACCTGGCTTCCGAGAGACTCCAGATCCAGCGACAGCTTTGTGTCGAGACG 711
DB	525 AGCTCTTACCTGGCTTCCGAGAGAGTTCCAGATCCAGCGACAGCTTTGTGTCGAGACG 466
QY	712 CTGTGCATGCGCGTGGAGCGGGTAGCAGCTGTTCATGTAGCGCCGGCGACGCGTTCGCGC 771
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QY	772 CCGGCATCCGCGCAGCATGGAAGTCTGAGTGGAGTGTTCATGGAAGTCCGCGCAACG 831
DB	405 CCGGCATCCGCGCAGCATGGAAGTCTGAGTGGAGTGTTCATGGAAGTCCGCGCAACG 346
QY	832 CAAGACTTGGCGCGAGATTTAGAGAAAGAGAGAAATTTTACCGTGTCTTCGGTTAATTGA 891
DB	345 CAAGACTTGGCGCGAGATTTAGAGAAAGAGAGAAATTTTACCGTGTCTTCGGTTAATTGA 286
QY	892 TTTGTTTTTCTCTCTGCGCGCATCTTGGACCGGAGGAGCATAGTAAGCAAGCAAGAG 951
DB	285 TTTGTTTTTCTCTCTGCGCGCATCTTGGACCGGAGGAGCATAGTAAGCAAGCAAGAG 226
QY	952 TGTCCATAGCGAATCATCAAGCAGAGAAACGCGAATCATGCGATGCGATGCGATGAGA 1011
DB	225 TGTCCATAGCGAATCATCAAGCAGAGAAACGCGAATCATGCGATGCGATGCGATGAGA 166
QY	1012 TGCAACCGATAGCTTTGATAGTAATTTTCTTTTAACTCTCTCTCTGATATGATAGAA 1071
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OY	1072	ACAAAGAGTACTGATTCGAAACCTGAGATCCCTTCTCAGCAATGCGAACTGGATCAT	1133
Db	105	ACAAAGAGTCAATGATTCGAAACCTGAGATCCCTTCTCAGCAATGCGCGC-AACTGGATCAT	47
OY	1132	CAGAAAA	1138
Db	46	CAGAAAA	40
RESULT 13			
CF988227			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PubMed			
COMMENT			
FEATURES			
Source			
Origin			
Query Match			
Best Local Similarity			
Matches			
OY	300	GGAAGACACATCATTCATCTCCACGAGCTGTTGGCAACAGATGATTCGCAATTGCGCG	359
Db	15	GCAAGAGGCATCATTCATCTCCACGAGCTGTTGGCAACAGATGATTCGCGC	74
OY	360	CAGTTCCCGGGGAGACGACAAAGATCAGAACGTTGTGGCACACCCACTTCAGAA	419
Db	75	CAGTTCCCGGGGAGACGACAAAGATCAGAACGTTGTGGCACACCCACTTCAGAA	134
OY	420	GCGCTCGATGCGCGGCTCAGGCGGATGTCGCGCGACGCGCGGCAAGAGACAA	479
Db	135	GCGCTCGATGCGCGGCTCAGGCGGATGTCGCGCGACGCGCGGCAAGAGACAA	194

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QY	600	CGGCAACGCGCGGATTCAGCTCGGCGTCGCGTCGCTGTCGCGCAAGAGAGAGCTCTT	659
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QY	660	CACCTCGGCTTCGAGGAGTTCAGATCGACGACAGCTTCTGATCGAGACGCTGTGCAT	719
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RESULT 14	LOCUS	DEFINITION
CK008265	CK008265	33406rxcgf_6875.y1 Oryza sativa cv. Pak6s particle sterile CDNA library Oryza sativa (indica cultivar-group) CDNA 5', mRNA sequence.

ACCESSION	CK008265
VERSION	CK008265.1
	GI:58597737

SOURCE ORGANISM	Oryza sativa (indica cultivar-group)	Oryza sativa (indica cultivar-group)

REFERENCE	1 (bases 1 to 509)
AUTHORS	Yu, J., Wang, J., Lin, W., Li, S., Li, H., Zhou, J., Ni, P., Dong, W.,

Hu, S., Zeng, C., Zhang, J., Zhang, Y., Li, R., Xu, Z., Li, S., Li, X., Zheng, H., Cong, L., Lin, L., Yin, J., Geng, J., Li, G., Shi, J., Liu, J., Lv, H., Li, J., Wang, J., Deng, Y., Ran, L., Shi, X., Wang, X., Wu, Q., Li, C., Reng, J., Wang, X., Li, D., Liu, D., Zhang, X., Ji, Z., Zhao, W., Sun, Y., Zhang, Z., Bao, J., Han, Y., Dong, L., Ji, J., Chen, P., Wu, S. and Liu, J.

TITLE The Genomes of *Oryza sativa*: A History of Duplications
JOURNAL Plos Biol. 3 (2), e38 (2005)

PUBMED 15685292
COMMENT Contact: Yan Zhou

Bioinformatics Department
Hangzhou Genomics Institute
No.51 Zhiliang Road, Hangzhou 310008, China
Tel.: 86-571-56605886
Fax: 86-571-56605884
Email: zhouyan@genomics.org.cn
Seq primer: MJ Forward
High quality sequence stop: 509
POLYA=No.

FEATURES	Location/Qualifiers
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QY	61	AGGGAAGAGCAAGCACAATG	GGGAGGCGTCCGTCCTG	GAGAGATGGGGCT	CAAAGAG	120
Db	73	AGGGAAGAGCAAGCACAATG	GGGAGGCGTCCGTCCTG	GAGAGATGGGGCT	CAAAGAG	132
QY	121	GSTCCATGAGCGCCGAGAGAG	ACAAGTCTCTCTCTGCCCA	TATCAGGCGCACCGGCCAC		180
Db	133	GSTCCATGAGCGCCGAGAGAG	ACAAGTCTCTCTCTGCCCA	TATCAGGCGCACCGGCCAC		192
QY	181	GGCACCTGGCGGCCCTGCTCC	CAAGCAACCGGGGCTGCTG	CTTGCGGCAAGAGCTTCCGG		240
Db	193	GGCACCTGGCGGCCCTGCTCC	CAAGCAACCGGGGCTGCTG	CTTGCGGCAAGAGCTTCCGG		252
QY	241	CTCCGGTGGATCAACTACCTG	CGCGCGGACATCAAGCGGGG	CACTTCTCCAAGAGAG		300
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QY	361	AGTTGCCCGGGAGGACGGA	CAACAGATCAAGACGTGTGG	CACACCACCTCAAGAG		420
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QY	481	AAAGCGAAGAGCGCGAA		497		
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LOCUS	500 bp	mRNA	linear	EST 06-FEB-2000
DEFINITION	Oryza sativa (japonica cultivar-group) supermixin Oryza			

sativa (japonica cultivar-group) cDNA clone 034-M012R-H01 3', mRNA sequence.

ACCESSION	CI175768
VERSION	CI175768.1
	GI:86535562

KEYWORDS EST.
SOURCE *Oryza sativa* (japonica cultivar-group)

ORGANISM *Oryza sativa* (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta

SpERMATOPHYTES; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
AUTHORS
1 (bases 1 to 500)
Kikuchi, S.

TITLE Collection and mapping of over 30,000 transcription units by the rice full-length cDNA project from japonica rice

JOURNAL Unpublished (2006)
COMMENT Contact: Shoshi Kikuchi

Department of Molecular Genetics, Head of Laboratory of Gene Expression

National Institute of Agrobiological Sciences
2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan

Tel: 81-29-838-7007
Fax: 81-29-838-7007

Email: skikuchi@nias.affrc.go.jp
This EST clone is one of 780k ESTs of Rice full length cDNA project

URL: http://cdna01.dna.afric.go.jp/cDNA/NIAS_Rice_Full-Length_cDNA_Project_Team:_Kikuchi,S.,_Satoh,K.

Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J.,
Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T.,

Ohneda, E., Yahagi, M., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Yamamoto, M., and Nakahama, Y.
FAIS Genome Sequencing & Analysis Group: Otsomo, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Narikawa, R., Nikiura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Teunode, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K., and Murakami, K.
Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carinci, P., Fukuda, S., Hanagata, K., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiroka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Otsu, N., Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Saeki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami, T., Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A., and Hayashizaki, Y.
Location/Qualifiers

FEATURES

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Best Local Similarity 100.0%; Pred. No. 1.9e-108;
Matches 493; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY      745 ATGGAGCCCGGGGAGCGCTTCGTCGCGCGCCCATCCGCGAGACATGAGACTACCTGCTC 804
Db      61  ATGGAGCCCGGGGAGCGCTTCGTCGCGCGCCCATCCGCGAGACATGAGACTACCTGCTC 120

OY      805 GGAGTCTTCATGAGAGTCCGCGAGCGCAAGACTTGCCGACAGTCTAGAGAAAGAGAGAG 864
Db      121 GGAGTCTTCATGAGAGTCCGCGAGCGCAAGACTTGCCGACAGTCTAGAGAAAGAGAGAG 180

OY      865 AATTTTACCGTTCTTCGTTAATTGATTGTTTCTCTCTCTGCGCCCATCTTGAC 924
Db      181 AATTTTACCGTTCTTCGTTAATTGATTGTTTCTCTCTCTGCGCCCATCTTGAC 240

OY      925 CGGAGGGACATAGCTAAGACAGACAGAGTCCATGAGCGAATCATCAAGAGAGAGAGC 984
Db      241 CGGAGGGACATAGCTAAGACAGAGTGTCCATGAGCGAATCATCAAGAGAGAGAGAGC 300

OY      985 CGAATCATGCGATGCGATGCGATGAGATGACCCAGTACCTTTGATAGTTAATTTTCTTT 1044
Db      301 CGAATCATGCGATGCGATGCGATGAGATGACCCAGTACCTTTGATAGTTAATTTTCTTT 360

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Db      361 TTTTACCTCTCTCTGTATGTATAGAAACAGAAAGATCATGATGAAACCTGAGATCC 420

OY      1105 TTTTCACAATGCAAACTGATCATGAAAAAGGGCTGCGCTTTCATTTGATTA 1164
Db      421 TTTTCACAATGCAAACTGATCATGAAAAAGGGCTGCGCTTTCATTTGATTA 480

OY      1165 ATTAATTCACACT 1177
Db      481 ATTAATTCACACT 493
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using bw model

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Title: US-10-521-811-1

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Scoring table: IDENTITY_NUC

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Searched: 5244920 seqs, 3466124231 residues

Total number of hits satisfying chosen parameters: 10469840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	744.6	61.9	774	9	ADA48651
5	744.6	61.9	774	11	ACL30325
6	420	34.9	454	10	ADL16949
7	420	34.9	454	10	ADK59612
8	375.2	31.2	1276	13	ADK59612
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22	314.2	26.1	662	12	AD142102	Ad142102 Plant tra
23	314.2	26.1	662	12	ADK02645	Adk02645 Corn orth
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26	302.8	25.2	643	12	AD142100	Ad142100 Plant tra
27	302.8	25.2	643	12	ADK02643	Adk02643 Rice orth
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ALIGNMENTS

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DT	20-NOV-2003	(first entry)
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DE	Rice gene conferring disease resistance in plants.	
XX	ADA48105;	
KW	disease resistance; pathogen tolerance; plant pathogen; ds; gene; plant.	
OS	Oryza sativa.	
XX	ADA48105;	
PN	WO2003000906-A2.	
XX	ADA48105;	
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PF	21-JUN-2002; 2002WO-1B002453.	
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PR	22-JUN-2001; 2001US-0300112P.	
XX	ADA48105;	
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XX	ADA48105;	
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PA	(SYGN) SYNGENTA PARTICIPATIONS AG.	
XX	ADA48105;	
PI	Glazebrook J, Briggs S, Cooper B, Goff SA, Moughamer T;	
XX	Katagiri F, Krepe J, Provart N, Rieke D, Zhu T;	
XX	WPI, 2003-184052/18.	
DR	P-PSDB; ADA48106.	
XX	ADA48105;	
PT	New polynucleotide comprising a plant nucleotide sequence having an open	
XX	reading frame that encodes a polypeptide associated with disease	
XX	resistance, useful for conferring resistance or tolerance to a plant	
XX	pathogen.	
XX	Claim 1; SEQ ID NO 175; 299pp; English.	
PS	The invention relates to a novel isolated polynucleotide comprising a	
XX	plant nucleotide sequence having an open reading frame that encodes a	
CC	plant nucleotide sequence having an open reading frame that encodes a	

CC polypeptide associated with disease resistance or its fragment having
CC substantially the same activity as the full-length polypeptide. The
CC polynucleotide of the invention is useful for conferring resistance or
CC tolerance to a plant pathogen. The present sequence represents a protein
CC conferring disease resistance used in the invention.

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Query Match 62.6%; Score 752.6; DB 9; Length 816;
Best Local Similarity 98.4%; Pred. No. 2.9e-139;
Matches 804; Conservative 0; Mismatches 4; Indels 9; Gaps 4;

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QY 79 ATGGGAGGAGGCTCCGTCGCGGAGAGATGGGGCTCAAGAGGGGTCCATGACGCCGAG 138
DB 1 ATGGGAGAGGCTCCGTCGCGGAGAGATGGGGCTCAAGAGGGGTCCATGACGCCGAG 60

QY 139 GAGGACAAAGTCTCTGTCGCCCATCATCAGCGCCACGCGCACTGGCGGCTTG 198
DB 61 GAGGACAAAGTCTCTGTCGCCCATCATCAGCGCCACGCGCACTGGCGGCTTG 120

QY 199 CCCAAGCAAGCC---GGGCTGCTGCTGTGGCGCAAGAGCTGCCGCTCCGTTGATCA 254
DB 121 CCCAAGCAAGCCGCGCAGGCTGCTGTGGCGCAAGAGCTGCCGCTCCGTTGATCA 180

QY 255 CTACCTGCGCGCGGACATCAAGCGGGGCAACTTCTCCAAAGAGAGAGAACCATCAT 314
DB 181 CTACCTGCGCGCGGACATCAAGCGGGGCAACTTCTCCAAAGAGAGAGAACCATCAT 240

QY 315 CCATCTCCACGAGCTGCTTGGCAA---CAGGTGTCGCGAATTGCGCGAGGTGCGCG 371
DB 241 CCATCTCCACGAGCTGCTTGGCAAAGCAGAGTGTGTCGCAATTGCGCGAGGTGCGCG 300

QY 372 GAGGACGAGCAACGAGATCAAGAACTGTGGCAC-ACCCACCTCAAGAGAGCGCTCGAT 430
DB 301 GAGGACGAGCAACGAGATCAAGAACTGTGGCACCAACCTCAAGAGAGCGCTCGATG 360

QY 431 CGCGGCTCAGGGCGGCTCATGTGCGCGGACGCGCGCAAGAGCAACAAGAGCCGAGA 490
DB 361 CGCGGCTCAGGGCGGCTCATGTGCGCGGACGCGCGCAAGAGCAACAAGAGCCGAGA 420

QY 491 GCGCGAAGAACGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 550
DB 421 GCGCGAAGAACGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 479

QY 551 CGTCTGCGGTGACGAGATCTCGATGAGCCTCGTCTGCGGTGCGAGAGGACGCGGCG 610
DB 480 CGTCTGCGGTGACGAGATCTCGATGAGCCTCGTCTGCGGTGCGAGAGGACGCGGCG 539

QY 611 GGATCAGCTCGGCGTCCGCGTCCGTTGGGCCAAGAGAGAGAGCTCTTCACTCGGCT 670
DB 540 GGATCAGCTCGGCGTCCGCGTCCGTTGGGCCAAGAGAGAGAGCTCTTCACTCGGCT 599

QY 671 CCGAGAGGTTCCAGATCGACGACAGCTTCTGTGCGAGACGCTGTGATGCGGCTGAGCG 730
DB 600 CCGAGAGGTTCCAGATCGACGACAGCTTCTGTGCGAGACGCTGTGATGCGGCTGAGCG 659

QY 731 GGTACACGTCCTCATGAGAGCCCGGAGAGCGCTTCTGTCGCGCGCATCGCGAGACA 790
DB 660 GGTACACGTCCTCATGAGAGCCCGGAGAGCGCTTCTGTCGCGCGCATCGCGAGACA 719

QY 791 TGGACTACTGCTCGAGAGTTCATGAGATCCGCGCAAGCGCAAGACTTGCAGATCT 850
DB 720 TGGACTACTGCTCGAGAGTTCATGAGATCCGCGCAAGCGCAAGACTTGCAGATCT 779

QY 851 AAGAAAGAGAGAGAAATTTTACCGTTTCTTGCTTAA 887
DB 780 AAGAAAGAGAGAGAAATTTTACCGTTTCTTGCTTAA 816
```

RESULT 2
ACL26123
ID ACL26123 standard; cDNA; 816 BP.
XX

AC ACL26123;
XX
XX 02-JUN-2005 (first entry)
XX
XX
DE Rice abiotic stress responsive polynucleotide SEQ ID NO:79.
XX
XX
KW ss; abiotic stress tolerance; transgenic plant; plant; cereal;
XX agriculture.

XX Oryza sativa.
OS
PN WO2003008540-A2.

PD 30-JAN-2003.

PF 21-JUN-2002; 2002MO-US019668.

PR 22-JUN-2001; 2001US-0300112P.

PR 24-AUG-2001; 2001US-031462P.

PR 26-SEP-2001; 2001US-0325277P.

PR 21-NOV-2001; 2001US-0332132P.

PA (SYGN) SYNGENTA PARTICIPATIONS AG.

PI Krepes J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F;

PI Moughamer T, Provart N, Rieke D, Zhu T;

DR WPI; 2003-248011/24.

PT New stress-responsive nucleic acid, useful for altering the

PT responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold

PT stress, salt stress or osmotic stress.

PS Claim 1; SEQ ID NO 79; 89pp; English.

XX
XX The invention relates to novel abiotic stress responsive polynucleotides
CC and polypeptides. Also disclosed are vectors, expression cassettes, host
CC cells, and plants containing such polynucleotides. Also disclosed are
CC methods for using the polynucleotides and polypeptides to alter the
CC responsiveness of a plant to abiotic stress. The invention is useful in
CC agriculture. The nucleic acid is useful for determining whether a test
CC plant has been exposed to an abiotic stress condition. It is also useful
CC for selecting an agent that alters abiotic stress regulated
CC polynucleotide expression in a plant cell, and to identify a homolog or
CC ortholog to an abiotic stress responsive polynucleotide. The nucleic acid
CC molecule and the polypeptide encoded by it are useful in altering the
CC responsiveness of a plant to an abiotic stress, such as cold stress, salt
CC stress, osmotic stress or any of their combinations. The present sequence
CC is used in the exemplification of the invention

SQ Sequence 816 BP; 164 A; 254 C; 280 G; 118 T; 0 U; 0 Other;

Query Match 62.6%; Score 752.6; DB 11; Length 816;
Best Local Similarity 98.4%; Pred. No. 2.9e-139;
Matches 804; Conservative 0; Mismatches 4; Indels 9; Gaps 4;

```
QY 79 ATGGGAGGAGGCTCCGTCGCGGAGAGATGGGGCTCAAGAGGGGTCCATGACGCCGAG 138
DB 1 ATGGGAGAGGCTCCGTCGCGGAGAGATGGGGCTCAAGAGGGGTCCATGACGCCGAG 60

QY 139 GAGGACAAAGTCTCTGTCGCCCATCATCAGCGCCACGCGCACTGGCGGCTTG 198
DB 61 GAGGACAAAGTCTCTGTCGCCCATCATCAGCGCCACGCGCACTGGCGGCTTG 120

QY 199 CCCAAGCAAGCC---GGGCTGCTGCTGTGGCGCAAGAGCTGCCGCTCCGTTGATCA 254
DB 121 CCCAAGCAAGCCGCGCAGGCTGCTGTGGCGCAAGAGCTGCCGCTCCGTTGATCA 180

QY 255 CTACCTGCGCGCGGACATCAAGCGGGGCAACTTCTCCAAAGAGAGAGAGAACCATCAT 314
DB 181 CTACCTGCGCGCGGACATCAAGCGGGGCAACTTCTCCAAAGAGAGAGAGAACCATCAT 240

QY 315 CCATCTCCACGAGCTGCTTGGCAA---CAGGTGTCGCGCAATTGCGCGAGGTGCGCG 371
```


DB 241 CCATCTCCACGAGCTCTTGGCAACAGAGTGTGCTCCGCAATTGCCGACAGTTCCCCCG 300
QY 372 GAGGACGCAACAGAGATCAAGAACTGTGGCAC-ACCCACTCAAGAAAGCGCTTGATG 430
DB 301 GAGGACGCAACAGAGATCAAGAACTGTGGCACAAACCCACTCAAGAAAGCGCTTGATG 360
QY 431 CGCGGCTCAGGCGGCTCATGTGCGCGGCAAGCGCGCAAGAAAGCAAGAAAGCGCAAG 490
DB 361 CGCGGCTCAGGCGGCTCATGTGCGCGGCAAGCGCGCAAGAAAGCAAGAAAGCGCAAG 420
QY 491 GCGGCAAGAAAGCGAGCT 550
DB 421 GCGGCAAGAAAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 479
QY 551 CGTCTCGGTGACGAGGCTCTGATGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 610
DB 480 CGTCTCGGTGACGAGGCTCTGATGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 539
QY 611 GGATCAGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCT 670
DB 540 GGATCAGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCT 599
QY 671 CCGAGGAGTTCCAGATCGACGACAGCTTCTGTGCGAGACGCTGATGCGCGCTGAGCG 730
DB 600 CCGAGGAGTTCCAGATCGACGACAGCTTCTGTGCGAGACGCTGATGCGCGCTGAGCG 659
QY 731 GGTACGAGCTGTTCATGAGAGCCCGGCGAGCGCTTCTGTGCGCGCGCATCGCGAGCA 790
DB 660 GGTACGAGCTGTTCATGAGAGCCCGGCGAGCGCTTCTGTGCGCGCGCATCGCGAGCA 719
QY 791 TGGACTACTGCTCGGAGCTTCATGAGAGCTTCGCGGCAAGCGCAAGCTTCCGCAATCT 850
DB 720 TGGACTACTGCTCGGAGCTTCATGAGAGCTTCGCGGCAAGCGCAAGCTTCCGCAATCT 779
QY 851 AGAGAAAGAGAGAGAAATTTTACCGTTTCTTCGCTTA 887
DB 780 AGAGAAAGAGAGAGAAATTTTACCGTTTCTTCGCTTA 816

RESULT 3
ADA69954
ID ADA69954 standard; DNA; 774 BP.
XX
AC ADA69954;
XX
DT 20-NOV-2003 (first entry)
XX
DE Rice gene, SEQ ID 3277.
XX
KM Plant; bacterial infection; fungal infection; viral infection; rice;
KW gene; ds.
OS
XX Oryza sativa.
OS
XX WO2003000898-A1.
XX
PD 03-JAN-2003.
XX
PF 22-JUN-2001; 2001WO-1B001105.
XX
PR 22-JUN-2001; 2001WO-1B001105.
XX
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
PI Katagiri F, Quan S, Tao Y, Whitman S, Xie Z, Zhu T, Zou G;
XX
DR MPI, 2003-175290/17.

Identifying at least one gene involved in plant resistance or response to
PT pathogenic infection for conferring resistance or tolerance to a plant to
PT bacterial, fungal or viral infection by determining or detecting plant

PT gene expression.
XX
PS Claim 6; SEQ ID NO 3277; 899bp; English.
XX
CC The present invention relates to a method (M1) for identifying genes
CC involved in plant resistance or response to pathogenic infection. M1
CC comprises identifying a gene whose expression is significantly altered in
CC the incompatible interaction of plant gene expression relative to
CC expression of the gene in an uninfected plant, in a mutant plant that
CC does not express a gene associated with response to pathogenic infection,
CC or in a corresponding incompatible or compatible interaction. (M1) is
CC useful for conferring resistance to resistance or tolerance to a plant to
CC bacterial, fungal or viral infection. The present sequence was used to
CC illustrate the invention.

Sequence 774 BP; 150 A; 248 C; 269 G; 107 T; 0 U; 0 Other;
SQ
Query Match 61.9%; Score 744.6; DB 8; Length 774;
Best Local Similarity 99.2%; Pred. No. 1.1e-137;
Matches 769; Conservative 0; Mismatches 4; Indels 2; Gaps 2;
QY 79 ATGGGAGGAGCTCCGCTGCTGCGAAGATGGGCTCAAGAGGCTCATGAGCCCGAG 138
DB 1 ATGGGAGGAGCTCCGCTGCTGCGAAGATGGGCTCAAGAGGCTCATGAGCCCGAG 60
QY 139 GAGGACAAAGTCTCTGCTGCGCCCAATCCAGCGCCAGCGCAACTGGCGCGCGCTG 198
DB 61 GAGGACAAAGTCTCTGCTGCGCCCAATCCAGCGCCAGCGCCAGCAACTGGCGCGCTG 120
QY 199 CCCAACAAGCCGGGCTGCTGCGTGGCGCAAGAGCTGCGGCTCCGCTGATCAACTAG 258
DB 121 CCCAACAAGCCGGGCTGCTGCGTGGCGCAAGAGCTGCGGCTCCGCTGATCAACTAG 180
QY 259 CTGCGGCCGCAATCAAGCGGGCAACTTCTCCAGAGAGAGAGCAACATCATCAT 318
DB 181 CTGCGGCCGCAATCAAGCGGGCAACTTCTCCAGAGAGAGAGCAACATCATCAT 240
QY 319 CTCCAAGAGCTCTGCGCAACAGGTGCTCGCAATTGCGCGCAAGTTCGCGGAGAGAG 378
DB 241 CTCCAAGAGCTCTGCGCAACAGGTGCTCGCAATTGCGCGCAAGTTCGCGGAGAGAG 300
QY 379 GACAAAGAGATCAAGAACTGTGGCAC-ACCCACTCAAGAAAGCGCTTGATGCGCGG 437
DB 301 GACAAAGAGATCAAGAACTGTGGCACAAACCCACTCAAGAAAGCGCTTGATGCGCGG 360
QY 438 TCAAGGCGGTCAATGTGCGCGGCAAGCGCGCAAGAAAGCAAGAGCCGAGCGGAA 497
DB 361 TCAAGGCGGTCAATGTGCGCGGCAAGCGCGGCAAGAAAGCAAGAGCCGAGCGGAA 420
QY 498 GAAAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCGTCTGTC 557
DB 421 GAAAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCGTCTGTC 479
QY 558 GGTGACGAGCTCTCGATGAGCTCTGCTGCTGCGGAGAGAGCAAGCAAGCGCGGATCAG 617
DB 480 GGTGACGAGCTCTCGATGAGCTCTGCTGCTGCGGAGAGAGCAAGCAAGCGCGGATCAG 539
QY 618 CTGCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGG 677
DB 540 CTGCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGG 599
QY 678 GTTCCAGATCGACGAGCTTCTGCTGCGGAGAGCGCTGATGAGCGCTGGAAGGATACGA 737
DB 600 GTTCCAGATCGACGAGCTTCTGCTGCGGAGAGCGCTGATGAGCGCTGGAAGGATACGA 659
QY 738 CGTGTCCATGAGCCCGGCGAGCGGCTTCTGCTGCGCGCCCATCGCGGAGCATGAGACTA 797
DB 660 CGTGTCCATGAGCCCGGCGAGCGGCTTCTGCTGCGCGCCCATCGCGGAGCATGAGACTA 719
QY 798 CTGCTCGAGAGTGTTCATGAGAGTCCGCGCAAGCGCAAGCTTGGCCGCAATCTAG 852
DB 720 CTGCTCGAGAGTGTTCATGAGAGTCCGCGCAAGCGCAAGCTTGGCCGCAATCTAG 774

RESULT 4
ADA48651
ID ADA48651 standard; DNA; 774 BP.
XX
AC ADA48651;
XX
DT 20-NOV-2003 (first entry)
XX
DE Rice gene conferring disease resistance in plants.
XX
KW disease resistance; pathogen tolerance; plant pathogen; ds; gene; plant.
XX
OS Oryza sativa.
XX
PN WO200300906-A2.
XX
PD 03-JAN-2003.
XX
PF 21-JUN-2002; 2002WO-IB002453.
XX
PR 22-JUN-2001; 2001US-0300112P.
XX
PR 26-SEP-2001; 2001US-0352277P.
XX
PR 22-MAR-2002; 2002US-0366535P.
XX
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
PI Glazebrook J, Briggs S, Cooper B, Goff SA, Moughamer T;
XX
PI Katagiri F, Krepe J, Provart N, Rieke D, Zhu T;
XX
DR MPI: 2003-184052/18.
XX
DR P-PSDB; ADA48652.
XX
PT New polynucleotide comprising a plant nucleotide sequence having an open
PT reading frame that encodes a polypeptide associated with disease
PT resistance, useful for conferring resistance or tolerance to a plant
PT pathogen.
XX
PS Claim 1; SEQ ID NO 721; 299pp; English.
XX
CC The invention relates to a novel isolated polynucleotide comprising a
CC plant nucleotide sequence having an open reading frame that encodes a
CC polypeptide associated with disease resistance or its fragment having
CC substantially the same activity as the full-length polypeptide. The
CC polynucleotide of the invention is useful for conferring resistance or
CC tolerance to a plant pathogen. The present sequence represents a gene
CC conferring disease resistance used in the invention.
XX
SO Sequence 774 BP; 150 A; 248 C; 269 G; 107 T; 0 U; 0 Other;
XX
Query Match 61.9%; Score 744.6; DB 9; Length 774;
Best Local Similarity 99.2%; Pred. No. 1.1e-137;
Matches 769; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

QY 379 GACAAAGGATCAAGAAAGTGTGGAC-ACCCACCTCAAGAGCGCTCGATGCGCGGC 437
DB 301 GACAAAGGATCAAGAAAGTGTGGACAAACCACTCAAGAGCGCTCGATGCGCGGC 360
QY 438 TCAGGCGGATGTCGCGGAGCGCGGCAAGAGCAAGAAAGCGGAAGCGCGGA 497
DB 361 TCAGGCGGATGTCGCGGAGCGCGGCAAGAGCAAGAAAGCGGAAGCGCGGA 420
QY 498 GAAGCCAGCG 557
DB 421 GAAGCCAGCG 479
QY 558 GGTGACGAGGTCCTGATGAGCTCGTCGATGCGAGAGAGCAAGCAAGCGCGGATCAG 617
DB 480 GGTGACGAGGTCCTGATGAGCTCGTCGATGCGAGAGAGCAAGCAAGCGCGGATCAG 539
QY 618 CTCGCGCTCCGCGCTCGTGTGCGCCAGAGAGAGCTTCCTTCACTTGGCTTCCGAGA 677
DB 540 CTCGCGCTCCGCGCTCGTGTGCGCCAGAGAGAGAGCTTCCTTCACTTGGCTTCCGAGA 599
QY 678 GTTCCAGATCGACGACAGCTTGTGTGCGAGAGAGCTGTGATGCGCGTGGAGGGTACGA 737
DB 600 GTTCCAGATCGACGACAGCTTGTGTGCGAGAGAGCTGTGATGCGCGTGGAGGGTACGA 659
QY 738 CGTGTCCATGAGAGCGCGGAGAGCGCTTGTGCGCGCGCATCGCGCGAGCATGGAAGCTA 797
DB 660 CGTGTCCATGAGAGCGCGGAGAGCGCTTGTGCGCGCGCATCGCGCGAGCATGGAAGCTA 719
QY 798 CTGAGCTCGAGAGTTCATGAGAGTCCGCGGAAGCGGAAGCTTCCGCGAGATCTAG 852
DB 720 CTGAGCTCGAGAGTTCATGAGAGTCCGCGGAAGCGGAAGCTTCCGCGAGATCTAG 774

RESULT 5
ACL30325
ID ACL30325 standard; cDNA; 774 BP.
XX
AC ACL30325;
XX
DT 02-JUN-2005 (first entry)
XX
DE Rice abiotic stress responsive polynucleotide SEQ ID NO:8503.
XX
DE ss; abiotic stress tolerance; transgenic plant; plant; cereal;
XX
KW agriculture.
XX
OS Oryza sativa.
XX
PN WO2003008540-A2.
XX
PD 30-JAN-2003.
XX
PF 21-JUN-2002; 2002WO-US019668.
XX
PR 22-JUN-2001; 2001US-0300112P.
XX
PR 24-AUG-2001; 2001US-0314662P.
XX
PR 26-SEP-2001; 2001US-0352277P.
XX
PR 21-NOV-2001; 2001US-0332132P.
XX
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
PI Krepe J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F;
XX
PI Moughamer T, Provart N, Rieke D, Zhu T;
XX
DR MPI: 2003-248011/24.
XX
PT New stress-responsive nucleic acid, useful for altering the
PT responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold
PT stress, salt stress or osmotic stress.
XX
PS Claim 1; SEQ ID NO 8503; 89pp; English.
XX

CC The invention relates to novel abiotic stress responsive polynucleotides
 CC and polypeptides. Also disclosed are vectors, expression cassettes, host
 CC cells, and plants containing such polynucleotides. Also disclosed are
 CC methods for using the polynucleotides and polypeptides to alter the
 CC responsiveness of a plant to abiotic stress. The invention is useful in
 CC agriculture. The nucleic acid is useful for determining whether a test
 CC plant has been exposed to an abiotic stress condition. It is also useful
 CC for selecting an agent that alters abiotic stress regulated.
 CC polynucleotide expression in a plant cell, and to identify a homolog or
 CC ortholog to an abiotic stress responsive polynucleotide. The nucleic acid
 CC molecule and the polypeptide encoded by it are useful in altering the
 CC responsiveness of a plant to an abiotic stress, such as cold stress, salt
 CC stress, osmotic stress or any of their combinations. The present sequence
 CC is used in the exemplification of the invention
 XX

Sequence 774 BP; 150 A; 248 C; 269 G; 107 T; 0 U; 0 Other;

Query Match 61.9%; Score 744.6; DB 11; Length 774;
 Best Local Similarity 99.2%; Pred. No. 1.1e-137;
 Matches 769; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

QY 79 ATGGGAGGGCTCCGCTGCGAGAAAGATGGGCTCAAGAGGGTCCATGACGCGGAG 138
 DB 1 ATGGGAGGGCTCCGCTGCGAGAAAGATGGGCTCAAGAGGGTCCATGACGCGGAG 60
 QY 139 GAGGACAAAGTCTCTGCTCCGACATCCAGCGGCGACGCGCAACTGGCGCGCTG 198
 DB 61 GAGGACAAAGTCTCTGCTCCGACATCCAGCGGCGACGCGCAACTGGCGCGCTG 120
 QY 199 CCCAAGCAAGCGGCGCTGCTGCGAGAGAGTGCAGGCTCCGCTGATCAATCA 258
 DB 121 CCCAAGCAAGCGGCGCTGCTGCGAGAGAGTGCAGGCTCCGCTGATCAATCA 180
 QY 259 CTGCGCGCGGACATCAAGCGGCGCACTTCTCCAGAGAGAGACACCATCATCAT 318
 DB 181 CTGCGCGCGGACATCAAGCGGCGCACTTCTCCAGAGAGAGACACCATCATCAT 240
 QY 319 CTCCAGAGCTGCTGGGCAAGGTGTCGCAATTGCGGCGGAGTGGCGCGGAGAG 378
 DB 241 CTCCAGAGCTGCTGGGCAAGGTGTCGCAATTGCGGCGGAGTGGCGCGGAGAG 300
 QY 379 GACAAAGAGATCAAGAACGTGTGGAC-ACCCACTCAAGAACGCTCGATCGCGGC 437
 DB 301 GACAAAGAGATCAAGAACGTGTGGACAAACCACTCAAGAACGCTCGATCGCGGC 360
 QY 438 TCAGGCGGCTCATGTTCGCGGCGAGCGGCGCAAGAACCAAGAGCCGAAGCGGAA 497
 DB 361 TCAGGCGGCTCATGTTCGCGGCGAGCGGCGCAAGAACCAAGAGCCGAAGCGGAA 420
 QY 498 GAAGCAGCG 557
 DB 421 GAAGCAGCG 479
 QY 558 GGTGACGAGTCTCGATGAGCTCTGCTGCGGAGAGAGCAAGCAAGCGCGGATCAG 617
 DB 480 GGTGACGAGTCTCGATGAGCTCTGCTGCGGAGAGAGCAAGCAAGCGCGGATCAG 539
 QY 618 CTGCGCGCTCGCGTCTGCTGCGGAGAGAGAGCTCTTCACTTGGCTTCGAGGA 677
 DB 540 CTGCGCGCTCGCGTCTGCTGCGGAGAGAGAGCTCTTCACTTGGCTTCGAGGA 599
 QY 678 GTTCCAGATCGAGCAGAGCTTCTGCTGCGGAGAGAGCTGCTGAGTCCGCTGAGAG 737
 DB 600 GTTCCAGATCGAGCAGAGCTTCTGCTGCGGAGAGAGCTGCTGAGTCCGCTGAGAG 659
 QY 738 CGTGTTCATGAGAGCGCGGAGCGCGTTCGCTGCGCGCGCATCGCGAGCATGAGACTA 797
 DB 660 CGTGTTCATGAGAGCGCGGAGCGCGTTCGCTGCGCGCGCATCGCGAGCATGAGACTA 719
 QY 798 CTGGCTCGAGAGTTCATGAGAGTCCGCGAGAGCGCAAGCTTGGCGGAGATCTAG 852
 DB 720 CTGGCTCGAGAGTTCATGAGAGTCCGCGAGAGCGCAAGCTTGGCGGAGATCTAG 774

RESULT 6
 ADD16949;
 ID ADD16949 standard; DNA; 454 BP.
 XX

AC ADD16949;
 XX

DT 15-JUN-2004 (first entry)
 XX

DE DNA (SeqID 1017) that confers an altered visual phenotype in plants.
 XX

XX de; visual phenotype; plant; architecture; leaf surface; chlorotic;
 XX bleaching; etching; wet leaf; stunting; elongation; texture;
 KM agronomic trait; growth regulation; dwarf variety; insect resistance;
 KM heat stress; transgenic.
 XX

XX Unidentified.
 XX

PN MO2003020741-A1.
 XX

PD 13-MAR-2003.
 XX

XX 30-AUG-2002; 2002MO-US027880.
 PF

XX 31-AUG-2001; 2001US-0316326P.
 PR

XX (DOWC) DOW CHEM CO.
 PA

XX (DOWC) DOW AGROSCIENTES LLC.
 PA

PI Crosley R, Skokut T, Ruegger M, Larrinua I, Shukla V;
 XX

DR WPI; 2003-300858/29.
 XX

XX Novel isolated nucleic acid derived from *Nicotiana benthamiana*, *Oryzae*
 PT sativa, *Saccharomyces cerevisiae*, and *Papaver rhoeas*, useful for
 PT conferring altered visual phenotypes in plants.
 XX

XX Claim 1; SEQ ID NO 1017; 517bp; English.

CC This invention relates to the identification and isolation of novel
 CC nucleic acid molecules that confer altered visual phenotypes in plants.
 CC Specifically, it refers to modifications of plant architecture and/or
 CC leaf surface features in plants, such as chlorotic, bleaching, etching,
 CC wet leaf, stunting, elongation and texture phenotypes, which are thought
 CC will be agronomic traits beneficial to the farmer. As such, these novel
 CC phenotypes can affect growth regulation i.e. useful for creating dwarf
 CC varieties, exhibit resistance to insects or heat stress, confer changes
 CC in pigment content such that plants have enhanced vitamin production or
 CC delayed senescence and also for example produce plants that control the
 CC production of ethylene. Furthermore, the present invention comprises
 CC generating transgenic plants, as well as reproducibly altering the visual
 CC phenotype of plant seeds, plant tissues and plant cells containing the
 CC polynucleotides described herein. This polynucleotide is a homologue of a
 CC DNA sequence that confers an altered visual phenotype when expressed in
 CC plants, the method of the invention.
 XX

Sequence 454 BP; 111 A; 147 C; 141 G; 55 T; 0 U; 0 Other;

Query Match 34.9%; Score 420; DB 10; Length 454;
 Best Local Similarity 98.8%; Pred. No. 1.6e-73;
 Matches 423; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAGCGGCTTCCTTCCAGAACACACACACGCAAGAGAGAGAGAGAGAGAGAGAG 60
 DB 27 CAGCGGCTTCCTTCCAGAACACACACACGCAAGAGAGAGAGAGAGAGAGAGAG 86

QY 61 AGGGAAG 120
 DB 87 AGGGAAG 146

QY 121 GGTTCATGAGAGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
 DB 147 GGTTCATGAGAGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 206

QY 181 GGCAACTGCGCGCCCTGCCCCCAAGCAAGCCGGGCTGCTGCTTGGCGCAAGAGCTGCCGG 240
 Db 207 GGCAACTGCGCGCCCTGCCCCCAAGCAAGCCGGGCTGCTGCTTGGCGCAAGAGCTGCCGG 266
 QY 241 CTCGGTGGATCACTACCTGCGCGCGGACATCAAGCGGGGCACTTCTCCAAAGAGAG 300
 Db 267 CTCGGTGGATCACTACCTGCGCGCGGACATCAAGCGGGGCACTTCTCCAAAGAGAG 326
 QY 301 GAGGACACCATCATCTCATCTCCAGAGCTGTTGGCAACAGGTGTGCGCAATTGCCGCC 360
 Db 327 GAGGACACCATCATCTCATCTCCAGAGCTGTTGGCAACAGGTGTGCGCAATTGCCGCC 386
 QY 361 AGTTGCCCCGGAGAGCAACGAGATCAAGAAAGTGTGGCACACCCCACTCAAGAG 420
 Db 387 AGTTGCCCCGGAGAGCAACGAGATCAAGAAAGTGTGGCACACCCCACTCAAGAG 446
 QY 421 CGCCTCGA 428
 Db 447 CGCCTCGA 454

RESULT 7

ADK59612
ID ADK59612 strand; DNA; 454 BP.

ADK59612;

06-MAY-2004 (first entry)

Plant DNA sequence which confers altered metabolic characteristic #6995.

altered metabolic characteristic; plant; acid metabolism;
 alcohol metabolism; fatty acid metabolism;
 branched fatty acid metabolism; alkaloid metabolism;
 amino acid metabolism; ester metabolism; glyceride metabolism;
 phenolic metabolism; carbohydrate metabolism; sterol metabolism;
 terpene metabolism; isoprenoid metabolism; alkene metabolism;
 alkyne metabolism; hydrocarbon metabolism; ketone metabolism;
 quinone metabolism; disease resistance; gene shuffling; sexual PCR; ds.

Unidentified.

MO2003020936-A1.

13-MAR-2003.

30-AUG-2002; 2002WO-US027884.

31-AUG-2001; 2001US-0316471P.

(DOMC) DOW CHEM CO.

(DOMC) DOW AGROSCIENCES LLC.

Weglarz T, Gachotte D, Blakelee B, McCreary DA, Pell RJ;

Oriedo JVB, Crosley R, Reddy AS, Shukla V, Larrina I, Miller BA;

WPI; 2003-313091/30.

Novel genes that confer altered metabolic characteristics in Nicotiana

benhamana plants, useful for altering the levels of metabolites e.g.

acids, fatty acids, amino acids, carbohydrates, hydrocarbons and sterols.

Claim 1; SEQ ID NO 6995; 2576bp; English.

The invention comprises DNA sequences which confer an altered metabolic
 characteristic when they are expressed in a plant. The DNA sequences of
 the invention are useful for producing plants with an altered metabolic
 characteristic, such as: altered acid metabolism, alcohol metabolism,
 fatty acid metabolism, branched fatty acid metabolism, alkaloid or other
 base metabolism, altered amino acid metabolism, altered ester metabolism,
 altered glyceride metabolism, altered phenolic metabolism, altered
 carbohydrate metabolism, altered sterol, oxygenated terpene, or

CC isoprenoid metabolism, alkene or alkyne metabolism, hydrocarbon
 CC metabolism, ketone or quinone metabolism. The DNA sequences of the
 CC invention may be used to provide disease resistance in a plant and gene
 CC shuffling or sexual PCR procedures. The present nucleic acid represents a
 CC DNA sequence of the invention.

Sequence 454 BP; 111 A; 147 C; 141 G; 55 T; 0 U; 0 Other;

Query Match 34.9%; Score 420; DB 10; Length 454;

Best Local Similarity 98.8%; Pred. No. 1.6e-73; Mismatches 5; Indels 0; Gaps 0;

Matches 423; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAGCCGCTCCCTTCCAGAAACACACAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
 Db 27 CAGCCGCTCCCTTCCAGAAACACACAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 86
 QY 61 AGGAG 120
 Db 87 AGGAG 146
 QY 121 GGTCCATGAGCGCGGAG 180
 Db 147 GGTCCATGAGCGCGGAG 206
 QY 181 GGCAACTGCGCGCCCTGCCCCCAAGCAAGCCGGGCTGCTGCTTGGCGCAAGAGCTGCCGG 240
 Db 207 GGCAACTGCGCGCCCTGCCCCCAAGCAAGCCGGGCTGCTGCTTGGCGCAAGAGCTGCCGG 266
 QY 241 CTCGGTGGATCACTACCTGCGCGCGGACATCAAGCGGGGCACTTCTCCAAAGAGAG 300
 Db 267 CTCGGTGGATCACTACCTGCGCGCGGACATCAAGCGGGGCACTTCTCCAAAGAGAG 326
 QY 301 GAGGACACCATCATCTCATCTCCAGAGCTGTTGGCAACAGGTGTGCGCAATTGCCGCC 360
 Db 327 GAGGACACCATCATCTCATCTCCAGAGCTGTTGGCAACAGGTGTGCGCAATTGCCGCC 386
 QY 361 AGTTGCCCCGGAGAGCAACGAGATCAAGAAAGTGTGGCACACCCCACTCAAGAG 420
 Db 387 AGTTGCCCCGGAGAGCAACGAGATCAAGAAAGTGTGGCACACCCCACTCAAGAG 446
 QY 421 CGCCTCGA 428
 Db 447 CGCCTCGA 454

RESULT 8

AD084500
ID AD084500 strand; cDNA; 1276 BP.

AD084500;

21-APR-2005 (first entry)

Plant full length insert polynucleotide seqid 3220.

plant protectant; plant growth regulant; gene therapy; plant;
 recombinant DNA construct; physical array; plant breeding marker;
 cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 extreme osmotic condition; pathogen tolerance; pest tolerance;
 growth rate; cell cycle pathway; disease resistance;
 galactomanan production; lignin production; plant growth regulator;
 yield; plant growth; plant development; seed oil; protein yield;
 protein content; gene; ss.

Unidentified.

US2004034888-A1.

19-FEB-2004.

28-APR-2003; 2003US-00425114.

06-MAY-1999; 99US-00304517.

```

PR 05-NOV-2001; 2001US-00985678.
XX
XX (LIU/) LIU J.
XX (ZHOU/) ZHOU Y.
XX (KOVA/) KOVALIC D K.
XX (SCRE/) SCREEN S E.
XX (TAB/) TABASKA J E.
XX (CAO/) CAO Y.
XX
XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX
XX WPI; 2004-180133/17.
XX
XX New recombinant DNA construct, useful for improving plant tolerance to
XX cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
XX pests, for conferring increased resistance to plant disease, or for
XX improving yield.
XX
XX Claim 1: SEQ ID NO 3220; 15pp; English.
XX
XX The invention describes a recombinant DNA construct comprising a
XX polynucleotide consisting of a sequence encoding an amino acid sequence
XX available in electronic form from the US patent office at
XX ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
XX of the invention are also useful in physical arrays of molecules and as
XX plant breeding markers. The recombinant DNA construct is useful for
XX improving plant tolerance to cold, heat, drought, herbicides, extreme
XX osmotic conditions, pathogens or pests, for manipulating growth rate in
XX plant cells by modification of the cell cycle pathway, for conferring
XX increased resistance to plant disease, for producing galactomannan,
XX lignin or plant growth regulators, for increasing the rate of homologous
XX recombination in plants, for improving yield by modification of
XX photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
XX or by providing improved plant growth and development under at least one
XX stress condition or for modifying seed oil or protein yield and/or
XX content. This sequence represents a plant full length insert
XX CC polynucleotide that can be used in the recombinant DNA construct of the
XX invention.
XX
XX Sequence 1276 BP; 290 A; 401 C; 392 G; 193 T; 0 U; 0 Other:
XX
XX Query Match 31.2%; Score 375.2; DB 13; Length 1276;
XX Best Local Similarity 64.6%; Pred. No. 1.4e-64;
XX Matches 711; Conservative 0; Mismatches 308; Indels 81; Gaps 7;
XX
XX QY 76 ACAATGGGAGGAGGCTCGTCTGCGAAGAAAGATGGGCTCAAGAGGCTCCATGAGACGCCG 135
XX DB 171 AGAATGGGAGAGCTCGTCTGCGAAGAAATGGGCTCAAGAGGCTCCATGAGACGCCG 230
XX QY 136 GAGGAGGAGAAAGTCTCTCGTCCCAATCCAGCCGCAAGGCGCAAGCTGAGCGCGC 195
XX DB 221 GAGGAGGAGAAATCTCTGTCGCAATCCAGAGCTTGGCGCACAGCAATGCGCGCG 290
XX QY 196 CTGCCCAAGCAAGCCGGGCTGCTGCTGCGGCAAGAGCTGCGGCTCCGATGATCAAC 255
XX DB 291 CTGCCCAAGCAAGCCGGGCTGCTGCTGCGGCAAGAGCTGCGGCTCCGATGATCAAC 350
XX QY 256 TACCTGCGGCGGAGCATCAAGCGGGCAACTTCTCCAGAGGAGAGAGACACCATCATC 315
XX DB 351 TACCTGCGGCGGAGCATCAAGCGGGCAACTTCTCCAGAGGAGAGAGACACCATCATC 410
XX QY 316 CATCTCCAGAGCTGTTGGCAACAGTGTCCGCAATTGCCGCGGTTGCCCGGAGAG 375
XX DB 411 ACCCTTCACAGAGCTGCGCAACAGTGTGTCCGATCGCGCGGCTGCCCGGCGG 470
XX QY 471 ACGGACCAAGAGATCAAGAACTGTGCAACAGCACTCAAGAAAGGCTGAGGCCACG 530
XX DB 435 -----GGCTCAGGCGGCTCATGTCTCGCGCGAGCGGC 465
XX QY 531 ACCAAGACAGCTGAGAGCAGAGCAGCAGGCGCGCATGTGTGATCGCCGCGCAGGAAG 590

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QY 466 GCGAAGACACAGAAGACCGAAGAGCGGGAAGAGCCGCGCGCGCGCGCGCGCG 525
XX 591 CGCAGACAGGCGCAAGCGCGGCGGAGTCCAGAGACAAAGACAGAGCGCGCGCGCGCGCG 650
DB 526 CCGGCGTCCGCGCAGGCGGCTCCGCTGCTGCGTGAAGAGTCTGATGAGCTGCTGCG 585
XX 651 GCCACCAACCGCGCGCGCGGCTGCTGCTGAGAGAGTCCGCGCGCGCTGCTGCTGAGTGC 710
DB 586 GTGCGGAGAGAGCAGCAGCAGCGCGGATCAGCTCGGCGTCCGCGTCCGTTGCCAG 645
XX 711 ACGGACAGAGAGCAGGAGAAACAGCGGAGCAGCT---CGCGCGGTTCCCAAGAGAGAG 767
DB 646 GAGAGAGCTCCCTCACTCCGCTCCGAGGAGTCCAGATCGACAGACGCTTGGTGC 705
XX 768 AGCTTACCTCGTCTCGAGAGCGCGCGAGAGTCCAGTTCCAGACAGACGTTCTGCTG 827
DB 706 GAGACGCTGCTGATGCGCGCTGAGCGGATGAGC-----TGTC 744
XX 828 GAGAGCTGCTCACTGCGCTGAGCAGCTTCCAGACGATCCCGCAGAGCGCTGCTGCTG 887
DB 745 ATGAGACCGCGCAGCGCGCTTCTGCGCGCCATCCG-----CGACGAC 789
XX 888 GCGCGCTTCCGCGCAGCGCTGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 947
DB 790 ATGGACTACTGCTGCGAGTGTTCATGAGAGTCCGCGAGCG---CAAGACTTCCGCGAG 846
XX 948 TTGGACTACTGCTGCGAGTGTTCATGAGAGTCCGCGAGCGCGACCAACAGCTGCGCAG 1007
DB 847 ATCTAGAG-----AAAGAGAGAAATTTTACGTTCTTCTGCTTATTGAT---TTGTT 897
XX 1008 GTTTAAGGCGCGCAGCGCGCGCGCGCGAGAAATTTTCAAGTTCCCTGCTAATGATTCA 1067
DB 898 TTTTCTCTCTGCGCGCATCTTGTGCACCGAGGAGATGCTAACAGACAGAGTGTCCA 957
XX 1068 CTCTTCTCTCTCTGCGCAGCTCTTGTGCAGATTTGAGGAGGAGCAGTCAATTAACAGC 1127
DB 958 TGAGCAATCATCAACAGAGAAAGCGCAATATGCGATGCGATGAGATGACG 1017
XX 1128 TAATTAATGAGAGGAGTGTGTGTTGAGAGCAGCAGAGATTTAGAGAAACAGCGCA 1187
DB 1018 CAGTACCTTTGATAGTTAAATTTTCTTTTAACTCTCTCTGATATGATAGAAAGAA 1077
XX 1188 CATGCATTGACATCTATCTCTGTTTGTCTTGTATTAATTAAGATGATGATGACAA 1247
DB 1078 GAGATCAGTATGAAACT 1097
XX 1248 GATATCGTATGAAACT 1267
XX
XX RESULT 9
XX ADI42105
XX ID ADI42105 standard; DNA; 1352 BP.
XX
XX AC ADI42105;
XX
XX 22-APR-2004 (first entry)
XX
XX DE Plant transcription factor polynucleotide #314.
XX
XX transgenic; plant; enhanced tolerance to abiotic stress;
XX glycoside tolerance; hormone sensitivity; disease resistance;
XX sugar sensing; flowering; flower structure; stem bifurcation;
XX branching pattern; apical dominance; trichome; stem morphology;
XX root growth; root hair; seed development; cell proliferation;
XX cell differentiation; premature senescence; necrosis; plant size;
XX leaf morphology; seed morphology; seed biochemistry; root anthocyanin;
XX plant anthocyanin; light response; shade avoidance; bioinformatic;
XX transcription factor; gene; ds.
XX
XX Zea mays.
XX OS
XX US2004019927-A1.
XX PN
XX

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PD 29-JAN-2004.
XX 25-FEB-2003; 2003US-00374780.
PF 18-APR-2001; 2001US-00837944.
XX (SHER/) SHERMAN B K.
XX (RIEC/) RIECHMAN J L.
XX (JIANG/) JIANG C.
XX (HEAR/) HEARD J E.
XX (HAAR/) HAAKE V.
XX (CREE/) CREELMAN R A.
XX (RATC/) RATCLIFFE O.
XX (ADAM/) ADAM L J.
XX (REUB/) REUBER T L.
XX (KEDD/) KEDDIE J.
XX (BROU/) BROUN P E.
XX (PIGR/) PILGRIM M L.
XX (DUBE/) DUBELL A N.
XX (PINE/) PINEDA O.
XX (YUGG/) YU G.
XX Shearn BK, Riechmann JL, Jiang C, Heard JE, Haake V;
XX Creelman RA, Ratcliffe O, Adam LJ, Reuber TL, Keddie J, Broun PE;
XX Pilgrim ML, Dubell AN, Pineda O, Yu G;
XX WPI; 2004-132245/13.
XX
XX New transgenic plant comprising a recombinant polynucleotide of any one
XX of more than 500 nucleotide sequences, useful in bioinformatic search
XX methods.
XX
XX Claim 1; SEQ ID NO 568; 435bp; English.
XX
XX The invention describes a transgenic plant comprising a recombinant
XX polynucleotide of any one of more than 500 nucleotide sequences fully
XX defined in the specification or its complement. The method of the
XX invention can be used to produce a plant having altered traits such as:
XX enhanced tolerance to abiotic stress; glyphosphate tolerance; hormone
XX sensitivity; disease resistance; sugar sensing; early or late flowering;
XX altered flower structure; change in stem bifurcations; altered branching
XX pattern; reduced apical dominance; reduced trichome density; lack of
XX trichomes; reduced ectopic trichome development; altered trichome
XX development; increase in trichome number; altered stem morphology;
XX increased root growth; increased root hairs; altered seed development;
XX altered cell proliferation or cell differentiation; rapid development;
XX premature senescence; increased necrosis; increase in seedling or plant
XX size; decreased plant size; leaf morphology; seed morphology; seed
XX biochemistry; increase in root anthocyanins; increase in plant
XX anthocyanins; or alteration in light response or shade avoidance. The
XX transgenic plant, polynucleotides and polypeptides are useful in
XX bioinformatic search methods. This sequence represents a plant
XX transcription factor, and an orthologue of Arabidopsis thaliana
XX transcription factors isolated in the invention, that can be used in the
XX creation of a transgenic plant with altered traits.
XX
XX Sequence 1352 BP; 300 A; 431 C; 414 G; 207 T; 0 U; 0 Other;
SQ
Query Match 31.2%; Score 375.2; DB 12; Length 1352;
Best Local Similarity 64.6%; Pred. No. 1.4e-64;
Matches 711; Conservative 0; Mismatches 308; Indels 81; Gaps 7;
QY 76 ACAATGGGAGGCTCCGTCGCGCAAGATGGGGCTCAAGAGGGTCCATGAGCGCG 135
DB 195 AAGATGGGAGGCTCCGTCGCGCAAGATGGGGCTCAAGAGGGGCTCAAGAGCGCG 254
QY 136 GAGGAGGAGCAAGCTCTCGTCGCGCCATCCAGCGCCAGCGCCAGCGCAACTGCGCGCC 195
DB 255 GAGGAGGAGCAAGATCTCTGTCGCGCCATCCAGAGCTTGGGCGCAAGCAACTGCGCGCG 314
QY 196 CTGCCCCAAGCAAGCGCGGCTGCTGCGTGGCGCAAGAGCTCGCGGCTCCGCTGATCAAC 255
DB 315 CTGCCCCAAGCAAGCGCGGCTGCTGCGTGGCGCAAGAGCTGCGGCTCCGCTGATCAAC 374

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QY 256 TACCTGGGCGCGGACATCAAGCGGGGCAACTTCTCCAGAGAGAGAGACATCATC 315
DB 375 TACCTGGGCGCGGACATCAAGCGGGGCAACTTCTCCAGAGAGAGAGACATCATC 434
QY 316 CATCTCCAGAGCTGCTTGGCAACAGTGTCTCCGAATTGCGCCAGGTTGCGGGAG 375
DB 435 ACCCTCCAGAGAGCTCGGCAACAGTGTCTCCGATCTGCGCCAGGCTGCGGGCG 494
QY 376 ACGGCAACGAGATTAAGAAAGTGTGCAACACCCCTTCMAAGAACCGCTCGATCGCC- 434
DB 495 ACGGCAACGAGATTAAGAAAGTGTGCAACACCCCTTCMAAGAACCGCTGAGCCAC 554
QY 435 -----GGCTCAGGCGGCTCATGTCGCGCGAGCGCG 465
DB 555 ACCAAGCAGCTGGAGACAGAGACAGACGCGGGCGCATGCAAGTGTGACGCGCCGCAAG 614
QY 466 GGCAGAAAGCAACAGAACCGGAAGACGGAAGAACAGCGCGCGCGCGCGCGCG 525
DB 615 CGCAGCAGGCGCCAGCGCGCGGCTGCGAGCAAGAGACGACGCGCGCGCGCGCG 674
QY 526 CCGGCGTGGCGCGAGCGGTCCGCTCTGCTGCTGAGAGGAGTCTCGATGGCCTCTG 585
DB 675 GCCACACCGCGCGCGCGCTGGAACGCTGCGCGCGCTGCTGCTGAGCCGAGTGC 734
QY 586 GTGGCGGAGAGACAGCGCAACGCGGATCAGCTCGCGCGCTCGCTGCGCGCAAG 645
DB 735 ACGGAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 791
QY 646 GAGGAGAGCTCTTCACTCGGCTTCCGAGAGATTCAGATGACGACGACGACTTGTGTC 705
DB 792 AGCTTCACTCGCTCTCGAGAGCGCGCGAGAGAGTTCAGTTCGACGACGACGCTGTC 851
QY 706 GAGAGCGTGTGATGCCCGCTGGAACGGGTACAGC-----TGTGC 744
DB 852 GAGAGCGTGTGATGCCCGCTGGAACGGGTACAGC-----TGTGC 911
QY 745 ATGAGCGCGCGGAGCGGCTTCTGCGCGCGCGCATCCG-----CGACGAC 789
DB 912 GCGCGGCTTCCGAGAGTGTGCGCGCGCTCTCTCTCTGTCGCGCGCGCGCGAG 971
QY 790 ATGACTACTGCTCGAGTGTTCATGAGATCGCGGAGAGCG-----CAGACTTCCGCGAG 846
DB 972 TTGACTACTGCTCGAGTGTTCATGAGATCGCGGAGAGCGCGCACCAACACTGCGCGAG 1031
QY 847 ATCTAGAG-----AAGAGAGAGATTTTACCGTTTCTGCTTAATTGAT---TGTGT 897
DB 1032 GTTTAGAGCGCGCACGCGCGCGCGAGAAATTTTCAAGTTCCTGCTTAATTGATTCGTT 1091
QY 898 TTTCTCTCTGCGCGCATCTTGGACCGGAGGACATAGCTTACAGACCAAGAGTGTCA 957
DB 1092 CTTTCTCTCTGCGCGCATCTTGGACCGGAGGACATAGCTTACAGACCAAGAGTGTCA 1151
QY 958 TGAGCGAATCATCAAGCAAGAAAGCGAATCATGCGATGCGATGCGATGATGACCC 1017
DB 1152 TAATTAAATAGAGGGGTGTGTGTGTGAGAGACCAAGAGATTTAGAGAAACCAAGCGCA 1211
QY 1018 CAGTAGCTTTGATTAATTTTCTTTTAACTCTCTCTGTAATGTAAGAAACAGAA 1077
DB 1212 CATGCCAATGCAATCATCTCTTTGTTGCTTCTTGTATTAAGATCATCATGACAA 1271
QY 1078 GAGATCAGTATGAAACCT 1097
DB 1272 GATATCGGTGATGAAACCT 1291

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RESULT 10
 AD002648
 ID AD002648 standard; cDNA; 1352 BP.
 XX
 AC AD002648;
 XX
 DT 01-JUL-2004 (first entry)

XX Corn orthologue of Thalecress transcription factor, cDNA #22.
DE
XX
XX Corn; transcription factor; ss; gene; plant; transgenic; abiotic stress;
XX cold tolerance; heat tolerance; drought; osmotic stress;
XX phosphate limitation; potassium limitation; nitrogen limitation;
XX hormone sensitivity; disease resistance; sugar sensing; seed germination;
XX flowering; inflorescence architectural change;
XX meristem cell differentiation; phylloclaxy; apical dominance;
XX trichome development; seed development; premature senescence;
XX delayed senescence; lethality; necrosis; plant size; leaf morphology;
XX seed morphology; secondary metabolism; light response; shade avoidance.
OS
XX
XX Zea mays.
XX
XX US2004045049-A1.
XX
XX
XX 04-MAR-2004.
XX
XX
XX 10-APR-2003; 2003US-00412699.
XX
XX 13-SEP-1999; 99US-00394519.
XX 21-JAN-2000; 2000US-00489376.
XX 17-FEB-2000; 2000US-00506720.
XX 22-MAR-2000; 2000US-00532591.
XX 22-MAR-2000; 2000US-00533029.
XX 22-MAR-2000; 2000US-00533030.
XX 22-MAR-2000; 2000US-00533392.
XX 22-MAR-2000; 2000US-00533648.
XX 06-APR-2000; 2000WO-US009448.
XX 16-NOV-2000; 2000US-00713994.
XX 27-MAR-2001; 2001US-00819142.
XX 17-APR-2001; 2001US-00837444.
XX 30-JAN-2002; 2002US-00958131.
XX 14-JUN-2002; 2002US-00171468.
XX 09-AUG-2002; 2002US-00225066.
XX 09-AUG-2002; 2002US-00225067.
XX 09-AUG-2002; 2002US-00225068.
XX 17-DEC-2002; 2002US-04341668.
XX 25-FEB-2003; 2003US-00374780.
XX
XX (ZHAN/) ZHANG J.
XX (FROM/) FROM M E.
XX (HEAR/) HEARD J E.
XX (RIEC/) RIECHMANN J L.
XX (ADAM/) ADAM L J.
XX (BROU/) BROUN P E.
XX (PINE/) PINEDA O.
XX (REUB/) REUBER T L.
XX (KEDD/) KEDDIE J S.
XX (YUNG/) YU G.
XX (JIAN/) JIANG C.
XX (SAMA/) SAMAH R S.
XX (PILG/) PILGRIM M L.
XX (CREE/) CREELMAN R A.
XX (DUBE/) DUBEL A N.
XX (RATC/) RATCLIFFE O.
XX (KUMI/) KUMIMOTO R.
XX (SHER/) SHERMAN B K.
XX
XX Zhang J, Fromm ME, Heard JE, Riechmann JL, Adam LJ, Broun PE,
XX Pineda O, Reuber TL, Keddie JS, Yu G, Jiang C, Samaha RS,
XX Pilgrim ML, Creelman RA, Dubel AN, Ratcliffe O, Kumimoto R,
XX Sherman BK;
XX
XX WPI, 2004-225755/21.
XX
XX New transgenic plant, useful in developing phenotypes with altered or
XX improved characteristic or trait.
XX
XX Claim 1; SEQ ID NO 1062; 213pp; English.
XX
XX The invention relates to a transgenic plant comprising a recombinant

CC polynucleotide having a polynucleotide sequence or its complementary
CC sequence comprising a sequence encoding a polypeptide, that initiates
CC transcription (i.e. a transcription factor) from Arabidopsis, Soybean,
CC Rice, Rape or Corn, comprising any of the sequences appearing as AD001568
CC -AD003527 or AD003530-AD003559. Also included are using a transgenic
CC plant to grow a progeny plant, an expression cassette (comprising a
CC constitutive, inducible or tissue-specific promoter and a recombinant
CC polynucleotide described above), a host cell comprising the expression
CC cassette, producing a modified plant having a modified trait, identifying
CC a factor that is modulated by or interacts with a polypeptide encoded by
CC the polynucleotide sequence and identifying at least one downstream
CC polypeptide sequence that is subject to a regulatory effect of any of
CC the polypeptides encoded by the polynucleotide described above. The
CC transgenic plant is useful for producing a plant that has an altered
CC trait e.g. an enhanced tolerance to abiotic stress (increased tolerance
CC to chilling, germination in cold conditions, freezing tolerance, tolerance
CC to heat, tolerance to drought, tolerance to osmotic stress, tolerance to
CC salt, tolerance to phosphate limitation, tolerance to potassium
CC limitation, decreased sensitivity to nitrogen limitation), altered
CC hormone sensitivity, reduced sensitivity to abscisic acid, an altered
CC response to ethylene, disease resistance, altered susceptibility to
CC Botrytis, altered susceptibility to Fusarium, altered susceptibility to
CC Erysiphe, altered susceptibility to Pseudomonas syringae, altered
CC susceptibility to Sclerotinia, altered sugar sensing, improved seed
CC germination and seedling vigor, early flowering, late flowering, extended
CC period of flowering, an inflorescence architectural change, a change in
CC stem bifurcations, a lack of a shoot meristem, reduced meristem cell
CC differentiation, altered phylloclaxy, altered branching pattern, reduced
CC apical dominance, reduced trichome density, ectopic trichome development,
CC altered trichome development, altered stem morphology, increased root
CC growth, increased root hairs, altered seed development, altered cell
CC proliferation/cell differentiation, premature senescence, delayed
CC senescence, lethality, increased necrosis, an increase in seedling or
CC plant size, decreased plant size, a change in leaf morphology, increased
CC altered leaf development, increased leaf size and mass, glossy leaves,
CC leaf cell expansion, change in seed morphology, altered seed coloration,
CC increased seed size, decreased seed size, altered seed shape, change in
CC leaf biochemistry, increased leaf wax, an alteration in leaf prenyl lipid
CC content, increased leaf insoluble sugars, decreased leaf insoluble
CC sugars, increased leaf anthocyanins, an alteration of leaf fatty acid
CC content, an alteration of leaf glucosinolate content, change in seed
CC biochemistry, an increase in seed oil content, decrease in seed oil
CC content, increase in seed fatty acid content, decrease in seed fatty acid
CC content, increase in seed protein content, decrease in seed protein
CC content, alteration in seed prenyl lipid content, increase in seed
CC sterols, upregulation of genes involved in secondary metabolism, increase
CC in root anthocyanins, increase in plant anthocyanins, and alteration in
CC light response or shade avoidance. The present sequence encodes an
CC orthologue of a thalecress transcription factor isolated from Corn.
XX
SQ Sequence 1352 BP; 300 A; 431 C; 414 G; 207 T; 0 U; 0 Other;
Query Match 31.2%; Score 375.2; DB 12; Length 1352;
Best Local Similarity 64.6%; Pred. No. 1.4e-64;
Matches 711; Conservative 0; Mismatches 308; Indels 81; Gaps 7;
QY 76 ACNATGGGAGGCGCTCCGCTGCGGAGAGATGGGGCTTAAGAAGGTCCATGAGCGCG 135
DB 195 AGAATGGGAGAGCTCCGCTGCGGAGAGATGGGGCTTAAGAAGGGGCGCATGAGCGCG 254
QY 136 GAGGAGCAAGAGTCTCGTCCGCAATCCAGCGCCACGCGCACGCACTGCGCGCC 195
DB 255 GAGGAGCAAGATCTGCTGCGCATCCAGAGCTTGGCCACAGCAACTGCGCGCG 314
QY 196 CTGCCCAAGCAAGCGGCGCTGCTGCGGTCGCGCAAGAGCTGCGGCTCCGATGATCAAC 255
DB 315 CTGCCCAAGCAAGCGGCGCTGCTGCGGTCGCGCAAGAGCTGCGGCTCCGATGATCAAC 374
QY 256 TACCTGGCGCGCGGAGATCAAGCGGCGCAACTTCTCCAGAGGAGAGAGCAACCATCAGC 315
DB 375 TACCTGGCGCGCGGAGATCAAGCGGCGCAACTTCTCCAGAGGAGAGAGCAACCATCAGC 434
QY 316 CATCTCCAGAGAGCTGCTGGCAACAGGTGTCGCGCAATTGCTCCGCAAGTTGCGCGGAGG 375


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435 ACCCTCCAGCAGACTCGGCAACAGTGTGTCCGCATCGCCGCAAGCTGCCGAGCGG 494
436 ACGCAACAAGAGTCAAGAACCTGTGTGACACCCACTTCAGAGAGCGCTCGATCGCC- 434
437 ACGGACAAAGAGTCAAGAACCTGTGTGACACCCACTTCAGAGAGCGCTCGATCGCC- 434
438 ACGGACAAAGAGTCAAGAACCTGTGTGACACCCACTTCAGAGAGCGCTCGATCGCC- 434
439 ACGGACAAAGAGTCAAGAACCTGTGTGACACCCACTTCAGAGAGCGCTCGATCGCC- 434
435 -----GGCTCAGGCGGCTCATGTGCGCGCGAGCGGC 465
555 ACCAAGCAGCTGGAGCAGAGAGCAGACGCGGGCGCATGTGAGTGTGAGCGCCGCAAG 614
466 GGCAGAAAGCAACAAGAGCGGAGAGCGGAGAAAGCCAGCGCGCGCGCGCGCGCG 525
615 CGCAGACAGGCGCCAGAGCGCGCGGTGTCAGAGAGAGAGAGAGAGAGAGAGAGAG 674
526 CGCGGCGCGCGCGAGCGGTGCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 585
675 GCGACACACGCGCGCGCGGTGCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 734
586 GTGGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 645
735 ACGGACAAAGAGTCAAGAACCTGTGTGACACCCACTTCAGAGAGCGCTCGATCGCC- 791
646 GAGGAGAGCTCCTTCACTCGGCTTCCGAGAGAGTTCAGAGTGCAGACAGCTTGTGTG 705
792 AGCTTCACTCGTCTCTCGAGAGCGCGCGAGAGAGTTCAGAGTGCAGACAGCTTGTGTG 851
706 GAGAGCTGTGTGATGCGCGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 744
852 GAGAGCTGTGTGATGCGCGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 911
745 ATGAGAGCGCGGAGAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 789
912 GCGCGGCTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 971
790 ATGAGCTGTGTGATGCGCGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 846
972 TTGAGCTGTGTGATGCGCGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1031
847 ATCTAGAG-----AAAGAGAGAGATTTTACCGCTTCTTCCGTTAATTGAT---TTGTT 897
1032 GTTGTAGAGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1091
898 TTTTCTCTCTCTGCGCGCATCTTGCACCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 957
1092 CTTTCTCTCTCTGCGCGCATCTTGCACCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1151
958 TGAGCGAATCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1017
1152 TAAATTAATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1211
1018 CAGTAGCTTGTAGTAAATTTTCTTTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 1077
1212 CATGCCATTGTGATCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1271
1078 GAGATCAGTATGAAAGCT 1097
1272 GATATCGGTATGAAAGCT 1291

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RESULT 11
AD31537
ID AD31537 standard; cDNA; 1280 BP.

AD31537;

21-APR-2005 (first entry)

Plant full length insert polynucleotide seqid 14357.

plant protectant; plant growth regulant; gene therapy; plant;

recombinant DNA construct; physical array; plant breeding marker;

cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;

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KM extreme osmotic condition; pathogen tolerance; pest tolerance;
KM growth rate; cell cycle pathway; disease resistance;
KM galactomannan production; lignin production; plant growth regulator;
KM yield; plant growth; plant development; seed oil; protein yield;
KM protein content; gene; ss.
OS Unidentified.
XX US2004034888-A1.
XX 19-FEB-2004.
XX 28-APR-2003; 2003US-00425114.
XX 06-MAY-1999; 99US-00304517.
XX 05-NOV-2001; 2001US-00985678.
XX (LIU/J) LIU J.
XX (ZHOU/Y) ZHOU Y.
XX (KOVA/J) KOVALIC D K.
XX (SCRE/J) SCREEN S E.
XX (TAB/A) TABASKA J E.
XX (CAO/Y) CAO Y.
XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX WPI: 2004-180133/17.
XX
XX New recombinant DNA construct, useful for improving plant tolerance to
XX cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
XX pests, for conferring increased resistance to plant disease, or for
XX improving yield.
XX Claim 1: SEQ ID NO 14357; 15pp: English.
XX
XX The invention describes a recombinant DNA construct comprising a
XX polynucleotide consisting of a sequence encoding an amino acid sequence
XX available in electronic form from the US patent office at
XX ftp://seedata.uspto.gov/sequence.html?docid:2004034888. The polynucleotide
XX of the invention are also useful in physical arrays of molecules and as
XX plant breeding markers. The recombinant DNA construct is useful for
XX improving plant tolerance to cold, heat, drought, herbicides, extreme
XX osmotic conditions, pathogens or pests, for manipulating growth rate in
XX plant cells by modification of the cell cycle pathway, for conferring
XX increased resistance to plant disease, for producing galactomannan,
XX lignin or plant growth regulators, for increasing the rate of homologous
XX recombination in plants, for improving yield by modification of
XX photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
XX or by providing improved plant growth and development under at least one
XX stress condition or for modifying seed oil or protein yield and/or
XX content. This sequence represents a plant full length insert
XX polynucleotide that can be used in the recombinant DNA construct of the
XX invention.
XX
XX Sequence 1280 BP; 275 A; 417 C; 391 G; 197 T; 0 U; 0 Other;
XX
XX Query Match 30.4%; Score 366; DB 13; Length 1280;
XX Best Local Similarity 65.7%; Pred No. 9.1e-63;
XX Matches 706; Conservative 0; Mismatches 270; Indels 99; Gaps 8;

```



```

DB 187 CAACCTGGCGCGCTCCCAAGAACCCGGCTTGCTGGGTGGGCAAGAGCTGCCGCT 246
QY 243 CCGGTGGATCAACTACCTGGCGCGGACATCAAGCCGGGCACTTCTCCAAAGAGAGA 302
DB 247 CCGGTGGATCAACTACCTGGCGCGGACATCAAGCCGGGCACTTCTCCAAAGAGAGA 306
QY 303 GGACACCATCATCTCACTCCAGAGCTGTGGCAACAGTGGTCCGCAATTGGCCCGCAG 362
DB 307 GGACGCGATCATAGCTCTCCAGAGAGCTGGCAACAGTGGTCCGCAATTGGCCCGCAG 366
QY 363 GTTGGCCGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 422
DB 367 GTTGGCCGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 426
QY 423 CCTCGATGC-----GCCGGCTCAAGGGCGGTGATGTGGCGCGGAGCGG 464
DB 427 CCTGGATCCACCAAGCAGAGAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 486
QY 465 CCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 500
DB 487 CCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 546
QY 501 GCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 560
DB 547 GACGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 606
QY 561 GACGAGTCTCTGATGAGCTCTGCTGGGCGAGAGAGAGAGAGAGAGAGAGAGAGAG 620
DB 607 GCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 666
QY 621 GCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 674
DB 667 GCGGAGCTGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 726
QY 675 GAGAGTTCAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 728
DB 727 GAGAGTTCAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 786
QY 729 GCGGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 760
DB 787 CACAGCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 846
QY 761 -----CGTTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 809
DB 847 GCGCGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 906
QY 810 GTTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 866
DB 907 GTTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 966
QY 867 TTTTACCGTTCTTCTGTTAAT-TGATTTGTTTTTCTCTCTCTCTCTCTCTCTCTCT 925
DB 967 AATTTTGGCTCTTAATGATTCATGTTCTTTCTCTCTCTCTCTCTCTCTCTCTCTCT 1026
QY 926 GGAGGAGATCTAGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 979
DB 1027 CTTGATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080

```

RESULT 12

AD142101 standard; DNM; 1344 BP.

AD142101;

22-APR-2004 (first entry)

Plant transcription factor polynucleotide #310.

transgenic; plant; enhanced tolerance to abiotic stress;
 KW glyophosphate tolerance; hormone sensitivity; disease resistance;
 KW sugar sensing; flowering; flower structure; stem bifurcation;

branching pattern; apical dominance; trichome; stem morphology;
 KW root growth; root hair; seed development; cell proliferation;
 KW cell differentiation; premature senescence; necrosis; plant size;
 KW leaf morphology; seed morphology; seed biochemistry; root anthocyanin;
 KW plant anthocyanin; light response; shade avoidance; bioinformatic;
 KW transcription factor; gene; ds.

Zea mays.

US2004019927-A1.

29-JAN-2004.

25-FEB-2003; 2003US-00374780.

18-APR-2001; 2001US-00837944.

(SHER/) SHERMAN B K.

(RIEC/) RIECHMANN J L.

(JIAN/) JIANG C.

(HEAR/) HEARD J E.

(HAAR/) HAARE V.

(CREE/) CREELMAN R A.

(RATC/) RATCLIFFE O.

(ADAM/) ADAM L J.

(REUB/) REUBER T L.

(KEDD/) KEDDIE J.

(BROU/) BROUD P E.

(PILG/) PILGRIM M L.

(DUBE/) DUBELL A N.

(PINE/) PINEDA O.

(YUGG/) YU G.

Sherman BK, Riechmann JL, Jiang C, Heard JE, Haake V,

Creelman RA, Ratcliffe O, Adam LJ, Reuber TL, Keddie J, Brown PE,

Pilgrim ML, Dubell AN, Pineda O, Yu G;

WPI; 2004-132245/13.

New transgenic plant comprising a recombinant polynucleotide of any one

of more than 500 nucleotide sequences, useful in bioinformatic search

methods.

Claim 1; SEQ ID NO 564; 435bp; English.

The invention describes a transgenic plant comprising a recombinant

polynucleotide of any one of more than 500 nucleotide sequences fully

defined in the specification or its complement. The method of the

invention can be used to produce a plant having altered traits such as:

enhanced tolerance to abiotic stress; glyophosphate tolerance; hormone

sensitivity; disease resistance; sugar sensing; early or late flowering;

altered flower structure; change in stem bifurcations; altered branching

pattern; reduced apical dominance; reduced trichome density; lack of

trichomes; reduced ectopic trichome development; altered trichome

development; increase in trichome number; altered stem morphology;

increased root growth; increased root hairs; altered seed development;

altered cell proliferation or cell differentiation; rapid development;

premature senescence; increased necrosis; increase in seedling or plant

size; decreased plant size; leaf morphology; seed morphology; seed

biochemistry; increase in root anthocyanins; increase in plant

anthocyanins; or alteration in light response or shade avoidance. The

transgenic plant, polynucleotides and polypeptides are useful in

bioinformatic search methods. This sequence represents a plant

transcription factor, and an orthologue of Arabidopsis thaliana

transcription factors isolated in the invention, that can be used in the

creation of a transgenic plant with altered traits.

Sequence 1344 BP; 306 A; 437 C; 401 G; 200 T; 0 U; 0 Other;

Query Match 30.4%; Score 366; DB 12; Length 1344;

Best Local Similarity 65.7%; Pred. No. 9, 1e-63; Indels 98; Gaps 8;

Matches 706; Conservative 0; Mismatches 270; Indels 98; Gaps 8;

[illegible]

RESULT 13
AD002644
ID AD002644 standard; cDNA, 1344 BP.
XX
AC ADO02644;
XX
DT 01-JUL-2004 (first entry)
XX
DE Corn orthologue of Thalecress transcription factor, cDNA #18.
XX
KW Corn; transcription factor; ss; gene; plant; transgenic; abiotic stress;
KW cold tolerance; heat tolerance; drought; osmotic stress;
KW phosphate limitation; potassium limitation; nitrogen limitation;
KW hormone sensitivity; disease resistance; sugar sensing; seed germination;
KW flowering; inflorescence architectural change;
KW meristem cell differentiation; phytoalexin; apical dominance;
KW trichome development; seed development; premature senescence;
KW delayed senescence; lethality; necrosis; plant size; leaf morphology;
KW seed morphology; secondary metabolism; light response; shade avoidance.
XX
OS Zea mays.
XX
PN US2004045049-A1.
XX
PD 04-MAR-2004.
XX
PF 10-APR-2003; 2003US-00412699.
XX
PR 13-SEP-1999; 99US-00394519.
PR 21-JAN-2000; 2000US-00489376.
PR 17-FEB-2000; 2000US-00506720.
PR 22-MAR-2000; 2000US-00533591.
PR 22-MAR-2000; 2000US-00533029.
PR 22-MAR-2000; 2000US-00533030.
PR 22-MAR-2000; 2000US-00533392.
PR 22-MAR-2000; 2000US-00533648.
PR 06-APR-2000; 2000US-00713994.
PR 16-NOV-2000; 2000US-00713994.
PR 27-MAR-2001; 2001US-00819142.
PR 17-APR-2001; 2001US-00837444.
PR 30-JAN-2002; 2002US-00956131.
PR 14-JUN-2002; 2002US-00171466.
PR 09-AUG-2002; 2002US-00225066.
PR 09-AUG-2002; 2002US-00225067.
PR 09-AUG-2002; 2002US-00225068.
PR 17-DEC-2002; 2002US-0431466P.
PR 25-FEB-2003; 2003US-00374780.
XX
XX (ZHAN/) ZHANG J.
PA (FROM/) FROMM M E.
PA (HEAR/) HEARD J E.
PA (RIEC/) RIECHMANN J L.
PA (ADAM/) ADAM L J.
PA (BROU/) BROUN P E.
PA (PINE/) PINEDA O.
PA (REUB/) REUBER T L.
PA (KEDD/) KEDDIE J S.
PA (YUGG/) YU G.
PA (JIANG/) JIANG C.
PA (SAMA/) SAMAHA R S.
PA (PIIG/) PILGRIM M L.
PA (CREE/) CREELMAN R A.
PA (DUBE/) DUBELL A N.
PA (RATC/) RATCLIFFE O.
PA (KUMI/) KUMIMOTO R.
PA (SHER/) SHERMAN B K.
XX
XX Zhang J, Fromm ME, Heard JE, Riechmann JL, Adam LJ, Broun PE;
PI Pineda O, Reuber TL, Keddie JS, Yu G, Jiang C, Samaha RS;
PI Pilgrim ML, Creelman RA, Dubell AN, Ratcliffe O, Kumimoto R;
PI Sherman B;
XX WPI: 2004-225755/21.

KM plant protectant; plant growth regulant; gene therapy; plant;
KM recombinant DNA construct; physical array; plant breeding marker;
KM cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KM extreme osmotic condition; pathogen tolerance; pest tolerance;
KM growth rate; cell cycle pathway; disease resistance;
KM galactomannan production; lignin production; plant growth regulator;
KM yield; plant growth; plant development; seed oil; protein yield;
KM protein content; gene; ss.

OS unidentified.

XX US2004034888-A1.

XX 19-FEB-2004.

XX 28-APR-2003; 2003US-00425114.

XX 06-MAY-1999; 99US-00304517.

XX 05-NOV-2001; 2001US-00985678.

XX (LIUJ/; LIU J.

XX (ZHOU/; ZHOU Y.

XX (KOVA/; KOVALIC D K.

XX (SCRE/; SCREEN S E.

XX (TAB/; TABASKA J E.

XX (CAO/; CAO Y.

XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;

XX WPI; 2004-180133/17.

XX New recombinant DNA construct, useful for improving plant tolerance to

XX cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or

XX pests, for conferring increased resistance to plant disease, or for

XX improving yield.

XX Claim 1; SEQ ID NO 24903; 15bp; English.

XX The invention describes a recombinant DNA construct comprising a

XX polynucleotide consisting of a sequence encoding an amino acid sequence

XX available in electronic form from the US patent office at

XX ftp://seedat.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide

XX of the invention are also useful in physical arrays of molecules and as

XX plant breeding markers. The recombinant DNA construct is useful for

XX improving plant tolerance to cold, heat, drought, herbicides, extreme

XX osmotic conditions, pathogens or pests, for manipulating growth rate in

XX plant cells by modification of the cell cycle pathway, for conferring

XX increased resistance to plant disease, for producing galactomannan,

XX lignin or plant growth regulators, for increasing the rate of homologous

XX recombination in plants, for improving yield by modification of

XX photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake

XX or by providing improved plant growth and development under at least one

XX stress condition or for modifying seed oil or protein yield and/or

XX content. This sequence represents a plant full length insert

XX polynucleotide that can be used in the recombinant DNA construct of the

XX invention.

XX Sequence 1126 BP; 239 A; 378 C; 360 G; 149 T; 0 U; 0 Other;

XX SQ

Query Match 29.3%; Score 352.6; DB 13; Length 1126;
Best Local Similarity 66.8%; Pred. No. 4e-60;
Matches 683; Conservative 0; Mismatches 224; Indels 116; Gaps 8;

QY 76 ACAATGGGAGGAGGCTCCGTCGTCGCGAAGATGGGGCTCAAGAAGGTCATGAGACGCCG 135

DB 74 ATAAATGGGAGGAGGCTCCGTCGTCGCGAAGATGGGGCTCAAGAAGGTCATGAGACGCCG 133

QY 136 GAGGAGCAAGAGTCTCTGTCGCGCCATCCAGCGCCAGCGCCAGCGCACTGCGCGCGC 195

DB 134 GAGGAGCAAGAGTCTCTGTCGCGCCATCCAGCGCTTGGCGCCAGCGCACTGCGCGCGG 193

QY 196 CTGCCCAAGCAAGCGCGGCTGCTGCGTTGCGGCAAGAGTGCCTGCGGTGATCAAC 255

DB 194 CTGCCCAAGCAAGCGCGGCTGCTGCGTTGCGGCAAGAGTGCCTGCGGTGATCAAC 253

QY 256 TACCTCGGCGCGGACATTAAGCGGGGCACTTTCTTCAAGAGAGAGAGACCACTCATC 315

DB 254 TACCTCGGCGCGGACATTAAGCGGGGCACTTTCTTCAAGAGAGAGAGAGAGAGAGAGAG 313

QY 316 CATCTCCAGAGCTGCTGGCAACAGAGTGTCCCGCAATTGCGCGCCAGAGTGGCCGGAGG 375

DB 314 AGCTTCAGAGAGCTGCGCAACAGAGTGTCCCGCAATTGCGCGCCAGAGTGGCCGGAGG 373

QY 376 ACGGCAACGAGATCAAGAACGCTGTGGCAACCACTTCAAGAAAGCGCTTCGATC--- 431

DB 374 ACGGCAACGAGATCAAGAACGCTGTGGCAACCACTTCAAGAAAGCGCTTCGATC--- 433

QY 432 -----GCCGCTCAAGGCGGATATGTCGCGGCGAAGGCGCGCAAGAGCAAC 477

DB 434 AAGCAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 493

QY 478 AAGGAGCCGAGAGAGCGCGAG-----AAGCCA 504

DB 494 AAGGAGCCGAGAGAGCGCGAG-----AAGCCA 553

QY 505 GCCG 555

DB 554 GACG 613

QY 556 TCGGTGAGAGAGTCTCTGATGAGCTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 615

DB 614 TCGGCG 673

QY 616 AGCTCGGCG 669

DB 674 AACGAGGAGAGTCTCTGATGAGCTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 733

QY 670 TCGGAGAGTCTCTGATGAGCTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 728

DB 724 GCCGAGAGTCTCTGATGAGCTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 793

QY 729 -----CGGCTAGAGAGTCTCTGATGAGCTCTGTCGTCGTCGTCGTCGTCGTCGTCG 760

DB 794 AGCTCGAGAGTCTCTGATGAGCTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 853

QY 761 -----CGTTCGTCG 807

DB 854 GTGCTGCG 913

QY 808 GTGCTGAGAGTCTCTGATGAGCTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 864

DB 914 GTGCTGAGAGTCTCTGATGAGCTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 973

QY 865 AATTTTACGATTTCTTGGTTAAT-----TGATTTGTTTCTCTCTGCGCGCATCT 919

DB 974 AGAATTTTCTGCTCTTAATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 1033

QY 920 TGCACCGAGAGGACATTAAGCAAGAGTGTCTAGAGCAATCATCAAGAGAGAA 979

DB 1034 TGCATCGAGAGGAGAGCAAGAGCAGCAGCTGATTTAAGAGAGAGAGAGAGAGAGAGAG 1093

QY 980 GAA 982

DB 1094 GAA 1096

RESULT 15

AD142104 standard; DNA, 1492 BP.

AD142104;

22-APR-2004 (first entry)

Plant transcription factor polynucleotide #313.

Db 1139 GAA 1141

Search completed: June 24, 2006, 19:33:39
Job time : 1462 secs

GenCore version 5.1.9
Copyright (C) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 25, 2006, 07:42:57 ; Search time 6808 Seconds
(without alignments) 11290.364 Million cell updates/sec

Title: US-10-521-811-1

Perfect score: 1202
Sequence: 1 cagcgcctccctcccaaga.....gtctaaaaaaaaaaaaaa 1202

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

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6: gb_ro:*
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8: gb_sy:*
9: gb_un:*
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11: gb_ov:*
12: gb_hcg:*
13: gb_in:*
14: gb_cm:*
15: gb_da:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1202	100.0	1202	4 OSMYB1202	Y11414 O. sativa mr
2	1192.8	99.2	1207	4 AY323484	Oryza sat
3	849	70.6	110000	4 AP008210_258	Continuation (259
4	849	70.6	139080	4 OSMYB1202	AL731616 Oryza sat
5	846	70.4	1836	4 AK111798	AX659818 Sequence
6	752.6	62.6	816	2 AX659818	AX653407 Sequence
7	744.6	61.9	774	2 AX653407	AX660354 Sequence
8	744.6	61.9	774	2 AX660354	AF467733 Oryza sat
9	546.4	45.5	673	4 AF467733	AY615199 Triticum
10	436.8	36.3	1044	4 AY615199	X99973 H. vulgare m
11	380.8	31.7	1180	4 HVMYB4TRF	AK112056 Oryza sat
12	326.6	27.2	1038	4 AK112056	AX653760 Sequence
13	284.2	23.6	672	2 AX653760	AY178579 Lolium pe
14	269.8	22.4	330	4 OSMYB1084	Y11350 O. sativa mr
15	269.2	22.4	1084	4 OSMYB1084	AK109011 Oryza sat
16	269.2	22.4	1326	4 AK109011	AX652852 Sequence
17	268.8	22.4	834	2 AX652852	AK108621 Oryza sat
18	251.8	20.9	1399	4 AK108621	

19	249	20.7	1637	4 AK11960	AK11960 Oryza sat
20	248.2	20.6	1163	4 AK107483	AK107483 Oryza sat
21	245.8	20.4	1023	2 AX652823	AX652823 Sequence
22	245.8	20.4	1528	4 AK111933	AK111933 Oryza sat
23	244.2	20.3	1665	4 AK111720	AK111720 Oryza sat
24	241.2	20.1	966	2 CS137754	CS137754 Sequence
25	234.8	19.5	1355	4 OSMYB1355	Y11415 O. sativa mr
26	234.8	19.5	1107	2 AX653762	AX653762 Sequence
27	223	19.4	1223	4 AY323480	AY323480 Oryza sat
28	221.4	19.3	1026	2 CS137758	CS137758 Sequence
29	228.2	19.0	1336	4 BT009312	BT009312 Triticum
30	227.6	18.9	1027	2 CS138020	CS138020 Sequence
31	227.6	18.9	1027	4 AK063027	AK063027 Oryza sat
32	225.8	18.8	1369	2 CS137822	CS137822 Sequence
33	225.6	18.8	1069	4 D88618	D88618 Oryza sativ
34	223.6	18.6	1139	4 AK106039	AK106039 Oryza sat
35	223.6	18.6	1450	4 AK111740	AK111740 Oryza sat
36	223.6	18.6	4669	4 AK121023	AK121023 Oryza sat
37	222.4	18.5	1601	2 ZM057002	U57002 Zea mays P
38	221.8	18.5	936	2 CS137814	CS137814 Sequence
39	221.6	18.4	1199	4 BT008981	BT008981 Triticum
40	220.8	18.4	1513	4 AF427146	AF427146 Zea mays
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42	220.4	18.3	1380	4 OSA311053	AJ311053 Oryza sat
43	220.4	18.3	1429	4 OSA311052	AJ311052 Oryza sat
44	219	18.2	1038	4 AF521880	AF521880 Zea mays
45	217.8	18.1	1389	4 AK064679	AK064679 Oryza sat

ALIGNMENTS

RESULT 1	OSMYB1202	1202 bp	mRNA	linear	PLN 18-APR-2005
LOCUS	O. sativa mRNA for myb factor, 1202 bp.				
DEFINITION	Y11414				
ACCESSION	Y11414.1 GI:1946264				
VERSION					
KEYWORDS	myb gene.				
SOURCE	Oryza sativa (japonica cultivar-group)				
ORGANISM	Oryza sativa (japonica cultivar-group)				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BBP				
	clade; Ehrhartoideae; Oryzaceae; Oryza.				
REFERENCE	1				
AUTHORS	Pandolfi, D., Solinas, G., Valle, G. and Coraggio, I.				
TITLE	The electronic Plant Gene Register				
JOURNAL	Plant Physiol. 114 (2), 747-749 (1997)				
PUBMED	9235602				
REFERENCE	2 (bases 1 to 1202)				
AUTHORS	Coraggio, I.				
TITLE	Direct Submission				
JOURNAL	Submitted (21-FEB-1997) I. Coraggio, Istituto Biosintesi Vegetali,				
	CNR, Via Bassini 15,, 20133, Milano, ITALY				
FEATURES	Location/Qualifiers				
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	/db_xref="GOA:O04140"				
	/db_xref="InterPro:IPR001005"				
	/db_xref="UniProtKB/TrEMBL:O04140"				

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ACCESSION	complete sequence.			
VERSION	AL731616			
KEYWORDS	AL731616.5 GI:57834148			
SOURCE	HTG.			
ORGANISM	Oryza sativa (japonica cultivar-group)			
REFERENCE	Oryza sativa (japonica cultivar-group)			
AUTHORS	Feng,Q., Zhang,Y., Hao,P., Wang,S., Fu,G., Huang,Y., Li,Y., Zhu,J., Liu,Y., Hu,X., Jia,P., Zhang,Y., Zhao,Q., Ying,K., Yu.S., Tang,Y.,			

TITLE
JOURNAL
PUBLISHED
REFERENCE
AUTHORS

Meng, Q., Zhang, L., Lu, Y., Mu, J., Lu, Y., Zhang, L.S., Yu, Z., Fan, D., Liu, X., Lu, T., Li, C., Wu, Y., Sun, T., Lei, H., Li, T., Hu, H., Guan, J., Wu, M., Zhang, R., Zhou, B., Chen, Z., Chen, L., Jin, Z., Wang, K., Yin, H., Cai, Z., Ren, S., Lv, G., Gu, W., Zhu, G., Tu, Y., Jia, J., Zhang, Y., Chen, J., Kang, H., Chen, X., Shao, C., Sun, Y., Hu, Q., Zhang, X., Zhang, W., Wang, L., Ding, C., Sheng, H., Gu, J., Chen, S., Ni, L., Zhu, F., Chen, W., Lan, L., Lai, Y., Cheng, Z., Gu, M., Jiang, J., Li, J., Hong, G., Xue, Y. and Han, B.

Sequence and analysis of rice chromosome 4
Nature 420 (6913), 316-320 (2002)

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Han, B., Feng, Q., Huang, Y.C., Li, Y., Zhu, J.J., Zhao, Q., Hu, X., Liu, Y.L., Mu, J., Yu, Z., Chen, L., Fan, D.L., Weng, Q.Q., Zhang, L., Lu, Y.Q., Yu, S.L., Liu, X.H., Lu, T.T., Zhang, Y.J., Lu, Y., Li, C., Li, T., Zhang, Y., Hu, H., Jia, P.X., Qian, Y.M., Ying, K., Zhou, B., Chen, Z.H., Hao, P., Zhang, H., Wu, M., Zhang, R.Q., Guan, J.P., Fu, G., Wang, S.Y., Ren, S.X., Lv, G., Lin, W., Gu, W.Q., Zhu, G.F., Tu, Y.F., Jia, J., Yin, H.F., Zhang, Y., Cai, Z., Chen, J., Kang, H., Chen, X.Y., Shao, C.Y., Sun, Y., Hu, Q.P., Zhang, X.L., Zhang, W., Wang, L.J., Ding, C.W., Sheng, H.H., Gu, J.L., Chen, S.T., Ni, L., Zhu, F.H. and Hong, G.F.

TITLE
JOURNAL

Submitted (04-MAY-2002) Han Bin, National Center for Gene Research, Chinese Academy of sciences, 500# Cao Bao Road, Shanghai 200233.
CHINA. E-mail enquiries: dhan@ncgr.ac.cn. Clone requests:
dhan@ncgr.ac.cn

Oryza sativa japonica (nipponbare) genomic DNA, chromosome 4, BAC clone: OSJNBa0073E02.

On Jan 14, 2005 this sequence version replaced gi:38568055.

Web site: http://www.ncgr.ac.cn

----- Summary Statistics -----
Assembly program: phrap

REMARK
COMMENT

This is a complete sequence.
Genes were identified by a combination of several methods: Gene prediction programs including Fgenesh (<http://www.softberry.com/>), genscan (<http://CCR-081.mit.edu/GENSCAN.html>), GenemarkKMM (<http://genemark.biology.matech.edu/genemark/>), tRNAscan-SE (Sean Eddy, <http://genome.wustl.edu/eddy/tRNAscan-SE/>), searches of the complete sequence against NCBI non-redundant protein database (nr) (<ftp://nbi.nlm.nih.gov/blast/db>) and the EST database at NCGR.

FEATURES
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CDS

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RESULT 5
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 REFERENCE
 AUTHORS
 1
 The Rice Full-length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-length cDNA Project Team; Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yasaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuka, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group; Ootomo, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Nikura, J., Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN, Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kondo, S., Komono, H., Miyazaki, A., Osato, N., Ota, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M., and Hayashizaki, Y.
 TITLE
 Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice
 JOURNAL
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 Adachi, J., Aizawa, K., Akiyama, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K.,

TITLE
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 JOURNAL

COMMENT

Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Komono, H., Kouda, M., Koya, S., Kuribara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakahama, Y., Nakamura, M., Namiki, T., Narikawa, R., Nikura, J., Nishi, K., Nomura, K., Nunasaki, R., Ohneda, E., Ohno, M., Ohtsuka, K., Oka, M., Ooka, H., Osato, N., Ota, Y., Ootomo, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yasaki, J., Yokomizo, S., and Yoshimura, A.
 Rice full-length cDNA
 Unpublished
 3 (bases 1 to 1836)

COMMENT

URL: <http://cdna01.dna.affrc.go.jp/cDNA/>
 NIAS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yasaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuka, K., Shishiki, T., Yamamoto, M., and Nakahama, Y.
 FAIS Genome Sequencing & Analysis Group: Ootomo, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobaishi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Narikawa, R., Nikura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K., and Murakami, K.
 Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akiyama, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Komono, H., Kouda, M., Koya, S., Kuribara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Nunasaki, R., Ohno, M., Osato, N., Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Shibata, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A., and Hayashizaki, Y.
 Location/Qualifiers
 1..1836

FEATURES

source
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 /cultivar="Nipponbare"
 /db_xref="taxon:39947"
 /clone="023105H16"

ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 6.7e-20;
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DB 1831 GCACGC 1836
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RESULT 5
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LOCUS AX659818 816 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 175 from Patent WO03000906.
ACCESSION AX659818
VERSION AX659818.1 GI:29161908
KEYWORDS
SOURCE
ORGANISM Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BBP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
AUTHORS Glaabrook, J., Briggs, S., Cooper, B., Goff, S. A., Moughamer, T.,
Katigiri, F., Krepe, J., Provart, N., Kicke, D. and Zhu, T.
TITLE Plant disease resistance genes

JOURNAL Patent: WO 03000906-A 175 03-JAN-2003;
Syngenta Participations AG (CH)
FEATURES
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Query Match 62.6%; Score 752.6; DB 2; Length 816;
Best Local Similarity 98.4%; Pred. No. 1.8e-177;
Matches 804; Conservative 0; Mismatches 4; Indels 9; Gaps 4;
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QY 139 GAGGACAAGTCTCTGTGCTGCCACATCCAGCGCCACGCGCACTGCGCGCTTG 198
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DB 61 GAGGACAAGTCTCTGTGCTGCCACATCCAGCGCCACGCGCACTGCGCGCTTG 120
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DB 121 CCMAAGCAAGCCGCGAGGAGCTGCTGCTGCGCAAGAGCTGCCGCTTCCGCTGATCA 180
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DB 181 CTACCTGCGCGCGGACATCAAGCGGCGCACTTCTCAAGAGAGAGAGACACCATCAT 240
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QY 315 CCATCTCAAGAGCTGCTTGGCA--CAGGTGCTCCCAATTGCCGCCAGGTTCCCGG 371
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DB 361 CGCGCGCTCAAGGCGGTGATGTCCGCGAGCGGCGGCAAGAGCAAGAAAGCGGAG 420
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RESULT 7
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LOCUS AX653407 774 bp DNA linear PAT 22-MAR-2003

DEFINITION	Sequence 3277 from Patent WO03000898.
ACCESSION	AX653407
VERSION	AX653407.1
KEYWORDS	GI:29156221
SOURCE	.
ORGANISM	Oryza sativa
	Oryza sativa
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE	1
AUTHORS	Chang, H.S., Chen, W., Cooper, B., Glazebrook, J., Goff, S.A., Hou, Y.M., Kaegebein, F., Quan, S., Tao, Y., Whitman, S., Xie, Z., Zhu, T. and Zou, G.
TITLE	Plant genes involved in defense against pathogens
JOURNAL	Patent: WO 03000898-A 3277 03-JAN-2003;
FEATURES	Syngenta Participations AG (CH)
source	location/Qualifiers
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Best Local Similarity	99.2%; Pmed. No.1.8e-175;
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Db	61	GAGGACAAAGTCTCTGTCGCCACATCCAGCGCCACCGCCACCGCACTGGCGCGCCCTG	120
Oy	199	CCCAAGCAAAGCCGGGCTGCTGCTGGCGGCAAGAGCTCCGGCTCCGGTGGATCAACTAC	258
Db	121	CCCAAGCAAAGCCGGGCTGCTGCTGGCGGCAAGAGCTCCGGCTCCGGTGGATCAACTAC	180
Oy	259	CTGCGGCGCGGACATCAAGCGGGGGCAACTTCTTCAAGAGAGAGAGAGACCATCATCATC	318
Db	181	CTGCGGCGCGGACATCAAGCGGGGGCAACTTCTTCAAGAGAGAGAGAGACCATCATCATC	240
Oy	319	CTCCACGAGCTGCTTGGCAACAGGTGTGCCGATTTGCCGCCAGGTGCCGGGAGAGCG	378
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Oy	379	GACAAACGAGATCAAGAAAGCTGTGGGAC-ACCACCTCAAGAAAGGCGCTCAATGGCGCGGC	437
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Oy	438	TCAGGGCGGTCAATGTCCGCGGAGCGGCGGCGCAAGAAAGCAAGAAAGCCGAAGCGCGAA	497
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Db	480	GATGACGAGAGTCTTGATGGACTCTCTCGTGGGCGGAGAGACACGGCAACGCGGGATCAG	539
Oy	618	CTCGGCGTTCGCGCTCCGTGTGCGCCAAAGAGAGAGCTTCTTCACTTCGCTTCCAGGA	677
Db	540	CTCGGCGTTCGCGCTCCGTGTGCGCCAAAGAGAGAGCTTCTTCACTTCGCTTCCAGGA	599
Oy	678	GTTCCAGATCGACGACAGCTTCTGATCGGAGACGCTGTCAATGCCGCTGGACGGATCGA	737
Db	600	GTTCCAGATCGACGACAGCTTCTGATCGGAGACGCTGTCAATGCCGCTGGACGGATCGA	659
Oy	738	CGTGTCAATGAGCCCGGCGACGCGTTCGTGCGCGCCATTCGCGCGACGATGAGACTA	797
Db	660	CGTGTCAATGAGCCCGGCGACGCGTTCGTGCGCGCGCCATTCGCGCGACGATGAGACTA	719

QY	798	852
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LOCUS	AX660364	774 bp	DNA	linear	PAT 22-MAR-2003
DEFINITION	Sequence 721 from Patent WO03000906.				
ACCESSION	AX660364				
VERSION	AX660364.1	GI:29162181			
KEYWORDS					
SOURCE					
ORGANISM	<i>Oryza sativa</i>				
REFERENCE	<i>Oryza sativa</i>				
AUTHORS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BER clade; Euhartioideae; Oryzaceae; Oryza.				
TITLE	Glazebrook, J., Briggs, S., Cooper, B., Goff, S.A., Moughamer, T., Katsagiri, F., Kreps, J., Provart, N., Riche, D. and Zhu, T.				
JOURNAL	Plant disease resistance genes Patent: WO 03000906-A 721 03-JAN-2003; Syngenta Participations AG (CH)				
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Best Local Similarity	99.2%; Pred. No. 1.8e-175;				
Matches	769; Conservative 0; Mismatches 4; Indels 2; Gaps 2;				
OY	79 ATGGGGAAGGCTCTCGTCTCGAGAAATGAGGCTCAAGAAAGGTTCATGAGCCGAG 138				
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DB	361 TCAGGGGGGTTCATTCGCGGCGAGCGGGCGGCAAGAAAGCAAGAAAGCGAAGCGCGAA 420				
OY	498 GAAGCCAGCTC 557				
DB	421 GAAGCCAGCTC 479				
OY	558 GGTACCGAGAGTCTCGAATGGCTGTGGTGGTGGCGAGAGAGACGCGGAGATCAG 617				
DB	480 GGTACCGAGAGTCTCGAATGGCTGTGGTGGTGGCGAGAGAGACGCGGAGATCAG 539				
OY	618 CTGGCGGCTCGCGCTCGGTGCGGCAAGAGAGAGAGCTCTTCACTTCGAGTTCCAGGA 677				

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O y	678	GTTCCAGATCGACGACAGCTTTGTGTCCGAGACGCTGTGCATGCGCGCTGAGCGGGTAGCA	737
D b	600	GTTCCAGATCGACGACAGCTTTGTGTCCGAGACGCTGTGCATGCGCGCTGAGCGGGTAGCA	659
O y	738	CGTGTCCATGAGACCCGGCGGACGCGTTGCTCGCGCCGCCATCCGCCGACGACATGGACTTA	797
D b	660	CGTGTCATGAGACCCGGCGGACGCGTTGCTCGCGCCGCCATCCGCCGACGACATGGACTTA	719
O y	798	CTGCGTCCGAGAGTTCATCGAGATCCGGCGCAACCGCAAGATTGGCCGAGATTCTAG	852
D b	720	CTGCGTCCGAGAGTTCATCGAGATCCGGCGCAACCGCAAGATTGGCCGAGATTCTAG	774

LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
AF467733	Oryza sativa myb protein mRNA, complete cds.	AF467733	AF467733.1	GI:18698671	Oryza sativa	Oryza sativa

REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES

1 (bases 1 to 673)
Yao,Q., Peng,R., Xiong,A., Li,X. and Fan,H.
Direct Submission
Submitted (14-JAN-2002) Bio-tech, Shanghai Academy of Agriculture
Science, Beidi Road 2201, Shanghai 201106, China
Location/Qualifiers

FEATURES	SOURCE	Location/Qualifiers
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ORIGIN

Query Match	45.5%	Score	546.4	DB 4	Length	673
Best Local Similarity	96.4%	Pred. NO.	8.9e-126			
Matches 623; Conservative	0	Mismatches	16		Indels	7
					Gaps	6

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Qy	62	GGAAGAGACAAACAATTGGGAGGGCTCCGTGCTGCAGAGAATTGGGGCTCAAGAAG	121
Db	62	GGAAGAGACAAACAATTGGGAGGGCTCCGTGCTGCAGAGAAGATTGGGGCTCAAGAAG	121
Qy	122	GTCCTATGACGCCGGAGAGAGACAAGGTCCTGTGGCCCATCTCAAGGCCACCGGCCAG	181
Db	122	GTCCTATGACGCCGGAGAGAGACAAGGTCCTGTGGCCCATCTCAAGGCCACCGGCCAG	181
Qy	182	GCAACTGGCGCGCCCTTGCCCAAGACCGGGCTCTGCGTTGCGGCAAGAGACTGCCGC	241
Db	182	GCAACTGGCGCGCCCTTGCCCAAGACCGGGCTCTGCGTTGCGGCAAGAGACTGCCGC	241
Qy	242	TCCGGTGATCAACTACTGCGCGCCGGACATCAAGCGGGCAAATTCTTCCAAGAGAGAG	301
Db	242	TCCGGTGATCAACTACTGCGCGCGGACATCAAGCGGGCAAATTCTTCCAAGAGAGAG	301

[illegible]

RESULT	10
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DEFINITION	Triticum aestivum transcription factor Myb2 (Myb2) mRNA, complete cds.
ACCESSION	AAG151199
VERSION	AAG151199.1 GI:47680446
KEYWORDS	
SOURCE	Triticum aestivum (bread wheat)

SOURCE	Triticum aestivum (bread wheat)
ORGANISM	Triticum aestivum
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta, Liliopsida; Poales; Poaceae; Bep clade; Pooidae; Triticeae; Triticum.
AUTHORS	1 (bases 1 to 1044)
TITLE	Chen, R., Ni, Z. and Sun, Q. The Isolation and Expression Analysis of the Myb Genes in Hexaploid Wheat (Triticum aestivum L.)
JOURNAL	unpublished
REFERENCE	2 (bases 1 to 1044)
AUTHORS	Chen, R., Ni, Z. and Sun, Q.
TITLE	Direct Submission
JOURNAL	Submitted (30-APR-2004) Department of Plant Genetics & Breeding,

FEATURES
SOURCE

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PVYSPDRSVSTLTSTSTASAAEHDHGGSGSASASVKECPLTSSSEEFQID
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I"

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ORIGIN

QY	314	TCATCTCCACGAGTCTTGCGACAGGAGTTCGGCAATTCGCGCGAGTTCCCGGGA	373
Db	232	TCAGCTGACACAGCTGCTCGGACAGATGCTCCGATTCGCGCAAGCTCCGCGGA	291
QY	374	GGACGACACGAGATCAAGAACGTGTGGACACCCACTCAAGAACGCGCTGATGCGC	433
Db	292	GGACGACACGAGATCAAGAACGTGTGGACACCCACTCAAGAACGCGCTGATGCGC	351
QY	434	CGGCTACGGGGCGGTCTGTTCGGCGGACGCGCGGCAAGAACCAAGAACCGGAG	489
Db	352	GGCGGACAGAGACGACAGAGAGAGCGCGCGCGCAAGAACGCGCGCGG	411
QY	490	-----AGCGGACAGA	499
Db	412	CGCGCGCGCGCGCGGACGCGGACGCGGACGCGGACGCGGACGCGGACGCGG	471
QY	500	AGCGACG	559
Db	472	CG	531
QY	560	TGACGAGTTC---TGATGCGCTGCTGCGGTGGCGGACGCGGACGCGGACGCGG	616
Db	532	TGACGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTC	591
QY	617	GCTCGCGCTGCGCGCTGCGGTGGCGGACGCGGACGCGGACGCGGACGCGG	673
Db	592	GCTCGCGCTGCGCGCTGCGGTGGCGGACGCGGACGCGGACGCGGACGCGG	651
QY	674	AGGAGTTCAGATCGACGACGCTTGTGTCGAGACGCTGTCGATGCGCTGAGCG	730
Db	652	AGGAGTTCAGATCGACGACGCTTGTGTCGAGACGCTGTCGATGCGCTGAGCG	711
QY	731	GGTACGAGTTCAGATCGACGACGCTTGTGTCGAGACGCTTGTGTCGATGCG	790
Db	712	TGACGAGTTCAGATCGACGACGCTTGTGTCGAGACGCTTGTGTCGATGCG	765
QY	791	TGAGTTCAGATCGACGACGCTTGTGTCGAGACGCTTGTGTCGATGCGCTGAG	826
Db	766	TGAGTTCAGATCGACGACGCTTGTGTCGAGACGCTTGTGTCGATGCGCTGAG	801
RESULT 12			
AK112056			
LOCUS	1038 bp	mRNA	linear
DEFINITION	Oryza sativa (japonica cultivar-group)	cdna clone:001-110-C03, full	
ACCESSION	AK112056		
VERSION	AK112056.1	GI:37988719	
KEYWORDS	FLI CDNA; oligo capping.		
SOURCE	Oryza sativa (japonica cultivar-group)		
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep		
REFERENCE			
AUTHORS	1		
	The Rice Full-length CDNA Consortium, National Institute of		
	Agrobiological Sciences Rice Full-length CDNA Project Team;		
	Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K.,		
	Kishimoto, N., Yasaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I.,		
	Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C.,		
	Ohtsuki, K., Shishiki, T., Foundation of Advancement of International		
	Science Genome Sequencing & Analysis Group; Ootomo, Y., Murakami, K.,		
	Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y.,		
	Kuroseki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M.,		
	Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Nishikura, J.,		
	Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J.,		
	Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN;		
	Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S.,		
	Hara, A., Hashidume, W., Hayatsu, N., Miyazaki, A., Ishii, Y., Itoh, M.,		
	Kagawa, I., Kondo, S., Kono, H., Miyazaki, A., Ootomo, Y., Ota, Y.,		
	Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shizaki, T.,		
	Yoshino, M., and Hayashizaki, Y.		
TITLE	Collection, mapping, and annotation of over 28,000 CDNA clones from		

JOURNAL
PUBMED
REFERENCE
AUTHORS

japonica rice
Science 301 (5631), 376-379 (2003)
12869764

TITLE
JOURNAL
REFERENCE
AUTHORS
JOURNAL

Unpublished
Rice full-length CDNA
3 (bases 1 to 1038)
Kikuchi, S.
Direct Submission
Submitted (12-SEP-2002) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki
305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp,
Tel:81-29-838-7007, Fax:81-29-838-7007)
This clone is one of the 32k full-length CDNA clones from japonica
rice.
URL: [COMMENT](http://cdna01.dna.affrc.go.jp/cDNA/NIAS_Rice_Full-length_CDNA_Project_Team_Kikuchi_S_Yasaki_J_Ishikawa_M_Yamada_H_Ooka_H_Hotta_I_Kojima_K_Namiki_T_Ohneda_E_Yahagi_W_Suzuki_K_Li_C_Ohtsuki_K_Shishiki_T_Yamamoto_M_and_Nakahama_Y_FAIR_Genome_Sequencing_and_Analysis_Group_Ootomo_Y_Iida_Y_Fujimura_T_Ikeda_R_Ishibiki_J_Kawamata_M_Kobayashi_M_Kodama_T_Kuroseki_T_Kusumegi_T_Lu_M_Masuda_H_Miura_J_Mizuno_K_Narikawa_R_Nishikura_J_Oka_M_Ryu_R_Sugano_S_Sugiyama_A_Suzuki_Y_Tsunoda_Y_Ueda_M_Xie_Q_Yokomizo_S_Yoshimura_A_Matsubara_K_and_Murakami_K_Genome_Exploration_Research_Group_in_Riken_Genomic_Sciences_Center_and_Genome_Science_Laboratory_in_Riken_Adachi_J_Aizawa_K_Akimura_T_Arakawa_T_Carninci_P_Fukuda_S_Hangaki_T_Hara_A_Hashizume_W_Hayashida_K_Hayatsu_N_Hizemoto_K_Hirooka_T_Hori_F_Iida_J_Iimura_K_Imotani_K_Ishii_Y_Itoh_M_Kagawa_I_Kanagawa_S_Katoch_H_Kawagashira_N_Kawai_J_Kobayashi_M_Kishikawa-Hirozane_T_Kojima_Y_Kondo_S_Kono_H_Kouda_M_Koya_S_Kuribara_C_Kuroseki_T_Kusumegi_T_Li_C_Lu_M_Masuda_H_Matsubara_K_Matsuyama_T_Miura_J_Miyazaki_A_Mizuno_K_Murakami_K_Murata_M_Nagata_T_Nakahama_Y_Nakamura_M_Namiki_T_Narikawa_R_Nishikura_J_Nishi_K_Nomura_K_Nunaseki_R_Ohneda_E_Ohno_M_Ohtsuki_K_Oka_M_Ooka_H_Osato_N_Ota_Y_Ootomo_Y_Ryu_R_Saitoh_H_Sakai_C_Sakai_K_Sakazume_N_Sano_H_Sasaki_D_Sato_K_Satoch_K_Shibata_K_Shinagawa_A_Shizaki_T_Shishiki_T_Sogabe_Y_Sugano_S_Sugiyama_A_Suzuki_K_Suzuki_Y_Tagamami_M_Tagamami_Takeda_Y_Tagawa_A_Takashi_F_Takaku-Akaiira_S_Tanaka_T_Tomaru_A_Toya_T_Tsunoda_Y_Ueda_M_Waki_K_Xie_Q_Yahagi_W_Yamada_H_Yamamoto_M_Yasunishi_A_Yasaki_J_Yokomizo_S_and_Yoshimura_A.</p>
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URL: [FEATURES](http://cdna01.dna.affrc.go.jp/cDNA/NIAS_Rice_Full-length_CDNA_Project_Team_Kikuchi_S_Yasaki_J_Ishikawa_M_Yamada_H_Ooka_H_Hotta_I_Kojima_K_Namiki_T_Ohneda_E_Yahagi_W_Suzuki_K_Li_C_Ohtsuki_K_Shishiki_T_Yamamoto_M_and_Nakahama_Y_FAIR_Genome_Sequencing_and_Analysis_Group_Ootomo_Y_Iida_Y_Fujimura_T_Ikeda_R_Ishibiki_J_Kawamata_M_Kobayashi_M_Kodama_T_Kuroseki_T_Kusumegi_T_Lu_M_Masuda_H_Miura_J_Mizuno_K_Narikawa_R_Nishikura_J_Oka_M_Ryu_R_Sugano_S_Sugiyama_A_Suzuki_Y_Tsunoda_Y_Ueda_M_Xie_Q_Yokomizo_S_Yoshimura_A_Matsubara_K_and_Murakami_K_Genome_Exploration_Research_Group_in_Riken_Genomic_Sciences_Center_and_Genome_Science_Laboratory_in_Riken_Adachi_J_Aizawa_K_Akimura_T_Arakawa_T_Carninci_P_Fukuda_S_Hangaki_T_Hara_A_Hashizume_W_Hayashida_K_Hayatsu_N_Hizemoto_K_Hirooka_T_Hori_F_Iida_J_Iimura_K_Imotani_K_Ishii_Y_Itoh_M_Kagawa_I_Kanagawa_S_Katoch_H_Kawagashira_N_Kawai_J_Kobayashi_M_Kishikawa-Hirozane_T_Kojima_Y_Kondo_S_Kono_H_Kouda_M_Koya_S_Kuribara_C_Matsuyama_T_Miyazaki_A_Murata_M_Nakamura_M_Nishi_K_Nomura_K_Nunaseki_R_Ohno_M_Osato_N_Ota_Y_Saitoh_H_Sakai_C_Sakai_K_Sakazume_N_Sano_H_Sasaki_D_Sato_K_Satoch_K_Shibata_K_Shinagawa_A_Shizaki_T_Shishiki_T_Sogabe_Y_Sugano_S_Sugiyama_A_Suzuki_K_Suzuki_Y_Tagamami_M_Tagamami_Takeda_Y_Tagawa_A_Takashi_F_Takaku-Akaiira_S_Tanaka_T_Tomaru_A_Toya_T_Waki_K_Yasunishi_A_and_Hayashizaki_Y.</p>
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Location/Qualifiers

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/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="001-110-C03"

ORIGIN

Query Match 27.2%; Score 326.6; DB 4; Length 1038;
 Best Local Similarity 71.0%; Pred. No. 1.1e-70;
 Matches 488; Conservative 0; Mismatches 169; Indels 30; Gaps 3;

77 CAATGGGAGGAGGCTCCGTCGTCGAGAGATGGGGCTCAAGAGGGTTCATGATCGCCG 136
 121 CATATGGGAGGAGGCTCCGTCGTCGAGAGATGGGGCTCAAGAGGGGCGGTGACGGCGG 180
 137 AGGAGGACAAAGTCTCTGTCGCCCAATCAGCGCCACGGCCACTGGCGCGCC 196
 181 AGGAGGACAAAGTCTCTGTCGCCCAATCAGCGCGCACAGCAACTGGCGCGCG 240
 197 TGGCCCAAGAGGCGGGGCTGCTGCTGGGGCAAGAGCTGGCGCTCCGGTGGATCACT 256
 241 TGGCCAGGAGGCGGGGCTTCTGCTGCGCAAGAGCTGGCGCTCCGGTGGATCACT 300
 257 ACTTGGGCGCGGACATCAAGCGGGGCACTTCTCAAGAGAGAGAGACCATCATCC 316
 301 ACTTGGGCGCGGACATCAAGCGGGGCACTTCAAGAGAGAGAGAGAGAGAGAGAG 360
 317 ATCTCCAGAGCTCTTGGCAACAGTGTCCGCAATTGGCCGAGTTGCCGGAGGA 376
 361 ACTTCCAGAGCTCTTGGCAACAGTGTCCGCAATTGGCCGAGTTGCCGGAGGA 420
 377 CGGACAAAGAGATCAAGAGCTGTGGCAACCCAGCTCAAGAGAGAGAGAGAGAGAG 433
 421 CGGACAAAGAGATCAAGAGCTGTGGCAACCCAGCTCAAGAGAGAGAGAGAGAGAG 480
 434 CGGCTCAGAGGCTCTATGTCGCGCGAGCGCGCGCAAGAGAGAGAGAGAGAGAGAG 493
 481 CGTCTCGCGCGCGAGAGCGCGCGCGCGCGCGCAAGAGAGAGAGAGAGAGAGAGAG 540
 494 CGAAGAGCGAGCG 553
 541 TGGCGGCTGCGAGTCCAGCTTCCGACCAAGCTGCGCGCGCGCGCGCGCGCGCGCG 600
 554 CGTCTCGAGAGAGTCTGATGAGTGGCTGCTGCGCGCGAGAGAGAGAGAGAGAGAG 613
 601 CCAGCAGAGAGTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 640
 614 TCAGCTCGAGCTCCGCGCTCGTGTGCGCGCAAGAGAGAGAGAGAGAGAGAGAGAG 673
 641 ----CTCGATGGGCTCTCCGGGAGATCAACAACAGAGAGAGAGAGAGAGAGAGAG 693
 674 AGGAGTTCCAGATCCAG 733
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 734 AGGAGTTCCAGATCCAG 760
 754 CGGACTCGGAGATGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780

RESULT 13
 AX653760 672 bp DNA linear PAT 22-MAR-2003
 DEFINITION Sequence 3630 from Patent WO03000898.
 ACCESSION AX653760
 VERSION AX653760.1 GI:29156574
 KEYWORDS
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BPP
 clade; Ehrhartoideae; Oryzaceae; Oryza.
 REFERENCE
 AUTHORS Chang, H.S., Chen, W., Cooper, B., Glazebrook, J., Goff, S.A., Hou, Y.M.,
 Katagiri, F., Quan, S., Tao, Y., Whitcham, S., Xie, Z., Zhu, T. and Zou, G.
 TITLE Plant gene involved in defense against pathogens
 JOURNAL Patent: WO 03000898-A 3630 03-JAN-2003;
 SynGene Participations AG (CH)
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 source Location/Qualifiers
 1..672

ORIGIN
 /organism="Oryza sativa"
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 /db_xref="taxon:4530"

Query Match 23.6%; Score 284.2; DB 2; Length 672;
 Best Local Similarity 71.6%; Pred. No. 4.9e-60;
 Matches 386; Conservative 1; Mismatches 149; Indels 3; Gaps 1;

79 ATGGGAGGAGGCTCCGTCGTCGAGAGATGGGGCTCAAGAGGGTTCATGAGCGCGGAG 138
 1 ATGGGAGGAGGCTCCGTCGTCGAGAGATGGGGCTCAAGAGGGGCGGTGACGGCGGAG 60
 139 GAGGAGAAAGTCTCTGTCGCCCAATCAGCGCCACGGCCACTGGCGCGCGCG 198
 61 GAGGAGAAAGTCTCTGTCGCCCAATCAGCGCGCACAGCAACTGGCGCGCGCG 120
 199 CCCAAGCAAGCGGGGCTGCTGCTGGCGCAAGAGCTGGCGCTCCGGTGGATCACTAC 258
 121 CCGAGGAGGCGGGGCTTCTGCTGCGCAAGAGCTGGCGCTCCGGTGGATCACTAC 180
 259 CTGGGCGCGGACATCAAGCGGGGCACTTCTCAAGAGAGAGAGAGAGAGAGAGAG 318
 181 CTCGCGCGCGGACATCAAGCGGGGCACTTCAAGAGAGAGAGAGAGAGAGAGAGAG 240
 319 CTCAGAGAGCTCTTGGCAACAGTGTCCGCAATTGGCCGAGTTGCCGGAGAGAG 378
 241 CTCAGAGAGCTCTTGGCAACAGTGTCCGCAATTGGCCGAGTTGCCGGAGAGAGAG 300
 379 GACAAAGAGATCAAGAGCTGTGGCAACCCAGCTCAAGAGAGAGAGAGAGAGAGAG 435
 301 GACAAAGAGATCAAGAGCTGTGGCAACCCAGCTCAAGAGAGAGAGAGAGAGAGAGAG 360
 436 GCTCAGAGGCTCTATGTCGCGCGAGCGCGCGCAAGAGAGAGAGAGAGAGAGAGAG 495
 361 TGTCTCGCGCGGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
 496 AAGAGAGAGCG 555
 421 GCGGTGGCATGAGCTTCCAGACCGTGGCTTCACTTGGAGAGAGATTCAGATC 480
 556 TCGGTGACAGAGTCTCTGATGAGCTGCTGCTGTCGCGAGAGAGAGAGAGAGAGAG 614
 481 GACGACAGCTTCTGTCGAGAGAGCTGTGCAATGACGCTGAGACAGCAGCATTCGGGAT 539

RESULT 14
 AY178579 330 bp mRNA linear PLN 18-JAN-2003
 DEFINITION Lolium perenne R2R3 MYB protein MYB4 (Myb4) mRNA, partial cde.
 ACCESSION AY178579
 VERSION AY178579.1 GI:27802511
 KEYWORDS
 SOURCE Lolium perenne
 ORGANISM Lolium perenne
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BPP
 clade; Pooideae; Poaceae; Lolium.
 REFERENCE
 AUTHORS Larsen, K.
 TITLE Cloning of MYB transcription factors expressed in stem tissue of
 perennial ryegrass
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 330)
 AUTHORS Larsen, K.
 TITLE Direct Submission
 JOURNAL Submitted (13-NOV-2002) Department of Crop Physiology and Soil
 Science, Danish Institute of Agricultural Sciences, Blichers Alle,
 Tjele DK-8830, Denmark
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 source Location/Qualifiers
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GenCore version 5.1.9
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590.475 Million cell updates/sec

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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1153	84.3	257	ADA48652	Ada48652 Rice prot
2	1153	84.3	257	ABM90166	Abm90166 Rice abio
3	827.5	60.5	258	ABJ10408	Abj10408 Myb-relat
4	827.5	60.5	258	ADH50100	Adh50100 Rice Myb-
5	799.5	58.4	257	AA654569	Aag54569 Zea mays
6	799.5	58.4	309	AA654568	Aag54568 Zea mays
7	762.5	55.7	162	ADA48106	Ada48106 Rice prot
8	762.5	55.7	162	ABM85964	Abm85964 Rice abio
9	747.5	54.6	248	AA654570	Aag54570 Zea mays
10	684	50.0	277	AD142106	Ad142106 Plant tra
11	669.5	48.9	278	AAW17811	Aaw17811 Tobacco M
12	661.5	48.4	385	AA641251	Aag41251 Arabidops
13	661.5	48.4	285	ADN72611	Adn72611 Thale cre
14	661.5	48.4	304	ADX91441	Adx91441 Plant ful
15	658	48.1	313	ADX71586	Adx71586 Plant ful
16	641.5	46.9	260	ADW17408	Adw17408 Eucalyptu
17	640	46.8	273	AAE01914	Aae01914 Arabidops
18	640	46.8	273	AAE01930	Aae01930 Arabidops
19	640	46.8	273	AAE02542	Aae02542 A. thalia
20	640	46.8	273	ADAI5585	Ada5585 A. thalia
21	640	46.8	273	ABO43123	AbO43123 A. thalia
22	640	46.8	273	ADD55700	Add55700 Thalecres
23	640	46.8	273	ADD30744	Add30744 Plant yle

24	640	46.8	273	8	AD141577	Ad141577 Plant tra
25	640	46.8	273	8	AD143515	Ad143515 Plant tra
26	640	46.8	273	8	AD003341	Ad003341 Thalecres
27	640	46.8	273	8	AD001751	Ad001751 Thalecres
28	640	46.8	273	8	AD001743	Ad001743 Thalecres
29	640	46.8	276	9	AD267575	Ad267575 Arabidops
30	628.5	45.9	246	5	AEC91871	Aec91871 Thale cre
31	626.5	45.8	139	5	ABJ10425	Abj10425 Myb-relat
32	626.5	45.8	139	8	ADH50134	Adh50134 Rice Myb-
33	623.5	45.6	246	8	AD001703	Ad001703 Thalecres
34	608	44.4	249	3	AA630515	Aag30515 Arabidops
35	606.5	44.3	276	3	AA641252	Aag41252 Arabidops
36	601	43.9	249	4	AAE02557	Aae02557 A. thalia
37	601	43.9	249	6	ADA15467	Ada15467 A. thalia
38	601	43.9	249	8	AD002409	Ad002409 Thalecres
39	597	43.6	249	3	AA626239	Aag626239 Arabidops
40	593	43.3	264	8	ADX94416	Adx94416 Plant ful
41	592	43.3	250	9	ADW17378	Adw17378 Eucalyptu
42	584	42.7	386	9	ADW17784	Adw17784 Pine rad
43	582	42.5	122	7	ABO43148	AbO43148 A. thalia
44	582	42.5	122	7	ADD55856	Add55856 Thalecres
45	563	41.2	481	9	ADW18468	Adw18468 Pinus rad

ALIGNMENTS

RESULT 1
ID ADA48652
ADA48652 standard; protein; 257 AA.
XX
AC ADA48652;
XX
DT 20-NOV-2003 (first entry)
XX
DE Rice protein conferring disease resistance in plants.
XX
KW disease resistance; pathogen tolerance; plant pathogen; plant; rice.
XX
OS Oryza sativa.
XX
PN WO2003000906-A2.
XX
PD 03-JUN-2003.
XX
PE 21-JUN-2002; 2002WO-IB002453.
XX
PR 22-JUN-2001; 2001US-0300112P.
PR 26-SEP-2001; 2001US-0352277P.
PR 22-MAR-2002; 2002US-0366535P.
XX
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
PI Glazebrook J, Briggs S, Cooper B, Goff SA, Moughamer T;
PI Katagiri F, Kreps J, Provart N, Riecke D, Zhu T;
PI WPI, 2003-184052/18.
DR N-PSDB; ADA48651.
XX
DR New polynucleotide comprising a plant nucleotide sequence having an open
PT reading frame that encodes a polypeptide associated with disease
PT resistance, useful for conferring resistance or tolerance to a plant
PT pathogen.
XX
PS Claim 10; SEQ ID NO 722; 299pp; English.
XX
CC The invention relates to a novel isolated polynucleotide comprising a
CC plant nucleotide sequence having an open reading frame that encodes a
CC polypeptide associated with disease resistance or its fragment having
CC substantially the same activity as the full-length polypeptide. The
CC polynucleotide of the invention is useful for conferring resistance or
CC tolerance to a plant pathogen. The present sequence represents a protein
CC conferring disease resistance used in the invention.

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XX SQ Sequence 257 AA;
Query Match      84.3%; Score 1153; DB 6; Length 257;
Best Local Similarity 84.1%; Pred. No. 6.4e-103;
Matches 222; Conservative 11; Mismatches 17; Indels 14; Gaps 3;

QY 1 MGRAPCCCKMGLKKGPWTPBEDKVLVAHIQRHGHGNWRLPQAGLLRCGKSCRRLMNY 60
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DB 1 MGRAPCCCKMGLKKGPWTPBEDKVLVAHIQRHGHGNWRLPQAGLLRCGKSCRRLMNY 60
QY 61 LRPDIKRGNFSKEEDTIIHLHLLGNRWSAIAARLPGRDNEIKNVWHTHLKKRLDAPA 120
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DB 61 LRPDIKRGNFSKEEDTIIHLHLLGNRWSAIAARLPGRDNGIKNVWH-----NPRQ 113
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QY 121 OGGHVAASG---GKHKKKPKSAKKPAAAA--AAPASPERASASSVTSSMASSVAEE 173
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DB 114 EAPRCAGSGRSCGRGERROAQAEBERERASRRRRPPASPERSASSSVTSSMASSVAEE 173
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QY 174 HGNAGISSASASVCAKEESSFTSASREFOIDSFMSSETLMPLDGYDVSMERGDAFVAPR 233
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DB 174 HGNAGISSASASVCAKEESSFTSASEEFOIDSFMSSETLMPLDGYDVSMERGDAFVAPR 233
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 234 SADMDYWLGVFMESGEAQLDLPQI 257
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 234 SADMDYWLGVFMESGEAQLDLPQI 257
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 2
ABM90166
ID ABM90166 standard; protein; 257 AA.
XX
XX ABM90166;
XX
XX 02-JUN-2005 (first entry)
XX
XX Rice abiotic stress responsive polypeptide SEQ ID NO:8888.
XX
XX abiotic stress tolerance; transgenic plant; plant; cereal; agriculture.
XX
XX Oryza sativa.
XX
XX WO2003008540-A2.
XX
XX 30-JAN-2003.
XX
XX 21-JUN-2002; 2002WO-US019668.
XX
XX 22-JUN-2001; 2001US-0300112P.
XX
XX 24-AUG-2001; 2001US-0314662P.
XX
XX 26-SEP-2001; 2001US-0325277P.
XX
XX 21-NOV-2001; 2001US-0332132P.
XX
XX (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
XX Kreps J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F,
XX
XX Moughamer T, Provart N, Rieke D, Zhu T,
XX
XX WPI; 2003-248011/24.
XX
XX New stress-responsive nucleic acid, useful for altering the
XX
XX responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold
XX
XX stress, salt stress or osmotic stress.
XX
XX Claim 1, SEQ ID NO 8888, 89pp; English.
XX
XX The invention relates to novel abiotic stress responsive polynucleotides
XX
XX and polypeptides. Also disclosed are vectors, expression cassettes, host
XX
XX cells, and plants containing such polynucleotides. Also disclosed are
XX
XX methods for using the polynucleotides and polypeptides to alter the
XX
XX responsiveness of a plant to abiotic stress. The invention is useful in
XX
XX agriculture. The nucleic acid is useful for determining whether a test
XX
XX plant has been exposed to an abiotic stress condition. It is also useful
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CC for selecting an agent that alters abiotic stress regulated
CC polynucleotide expression in a plant cell, and to identify a homolog or
CC ortholog to an abiotic stress responsive polynucleotide. The nucleic acid
CC molecule and the polypeptide encoded by it are useful in altering the
CC responsiveness of a plant to an abiotic stress, such as cold stress, salt
CC stress, osmotic stress or any of their combinations. The present sequence
CC is used in the exemplification of the invention
XX
XX SQ Sequence 257 AA;
Query Match      84.3%; Score 1153; DB 7; Length 257;
Best Local Similarity 84.1%; Pred. No. 6.4e-103;
Matches 222; Conservative 11; Mismatches 17; Indels 14; Gaps 3;

QY 1 MGRAPCCCKMGLKKGPWTPBEDKVLVAHIQRHGHGNWRLPQAGLLRCGKSCRRLMNY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 MGRAPCCCKMGLKKGPWTPBEDKVLVAHIQRHGHGNWRLPQAGLLRCGKSCRRLMNY 60
QY 61 LRPDIKRGNFSKEEDTIIHLHLLGNRWSAIAARLPGRDNEIKNVWHTHLKKRLDAPA 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 LRPDIKRGNFSKEEDTIIHLHLLGNRWSAIAARLPGRDNGIKNVWH-----NPRQ 113
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 OGGHVAASG---GKHKKKPKSAKKPAAAA--AAPASPERASASSVTSSMASSVAEE 173
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 114 EAPRCAGSGRSCGRGERROAQAEBERERASRRRRPPASPERSASSSVTSSMASSVAEE 173
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 174 HGNAGISSASASVCAKEESSFTSASREFOIDSFMSSETLMPLDGYDVSMERGDAFVAPR 233
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 174 HGNAGISSASASVCAKEESSFTSASEEFOIDSFMSSETLMPLDGYDVSMERGDAFVAPR 233
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 234 SADMDYWLGVFMESGEAQLDLPQI 257
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 234 SADMDYWLGVFMESGEAQLDLPQI 257
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 3
ABJ10408
ID ABJ10408 standard; protein; 258 AA.
XX
XX ABJ10408;
XX
XX 21-NOV-2002 (first entry)
XX
XX Myb-related transcription factor protein SEQ ID No 4.
XX
XX Myb; Myb-related transcription factor; plant; transgenic plant.
XX
XX Oryza sativa.
XX
XX US2002066120-A1.
XX
XX 30-MAY-2002.
XX
XX 19-NOV-1999; 99US-00443704.
XX
XX 20-NOV-1998; 98US-0109294P.
XX
XX (CAHO/) CAHOON R E.
XX
XX (LITUZ/) LITU Z.
XX
XX (ODEL/) ODEL J T.
XX
XX (RAFA/) RAFALSKI J A.
XX
XX (SHIJ/) SHI J.
XX
XX (WENG/) WENG Z.
XX
XX Cahoon RE, Liu Z, Odell JT, Rafalski JA, Shi J, Weng Z;
XX
XX WPI; 2002-556780/59.
XX
XX N-PSDB; ABR08112.
XX
XX Novel isolated polynucleotide useful for obtaining a nucleic acid
XX
XX fragment encoding a Myb-related transcription factor polypeptide.
XX
XX Claim 10; Page 15-16; 51pp; English.
```

XX The invention relates to a novel isolated polynucleotide comprising a
 CC first nucleotide encoding a polypeptide of 217, 120, or 268 amino acids
 CC that has 85%, 95%, or 96% identity based on the Clustal method of
 CC alignment when compared to a polypeptide selected from Myb polypeptides
 CC sequences of 128, 258, or 268 amino acids fully defined in the
 CC specification, or a second nucleotide sequence comprising the complement
 CC of the first nucleotide. The isolated polynucleotide is useful for
 CC obtaining a nucleic acid fragment encoding an Myb-related transcription
 CC factor polypeptide by using it to probe cDNA or genomic libraries. A
 CC nucleic acid fragment obtained using the isolated polynucleotide is
 CC useful to isolate cDNAs and genes encoding homologous proteins from the
 CC same or other plant species. The nucleic acid fragment is also useful to
 CC create transgenic plants in which the Myb-like protein is present at
 CC higher or lower levels than normal or in cell types. This sequence
 CC represents the protein of an Myb-related transcription factor of the
 CC invention

SO Sequence 258 AA;

Query Match 60.5%; Score 827.5; DB 5; Length 258;
 Best Local Similarity 62.1%; Pred. No. 2.3e-71;
 Matches 169; Conservative 29; Mismatches 45; Indels 29; Gaps 8;

QY 1 MGRAPCCCKMGLKKGWPTBEDKVLVAHIORHGNWRALPRQAGLLRCGKSCRLWIMY 60
 DB 1 MGRAPCCCKMGLKKGWPTBEDKVLVAHIORHGNWRALPRQAGLLRCGKSCRLWIMY 60
 QY 61 LRPDIRKGNFSEEDTIIHLHELGNRWSAIAARLPGRDNEIKVWHTLKKRLDAPA 120
 DB 61 LRPDIRKGNFSEEDTIIHLHELGNRWSAIAARLPGRDNEIKVWHTLKKRLDAPA 120
 QY 121 OGGHVAAGCGKKHKPKSAKKPAAAAA-----PASPERASSSVTSSMASSVAEEH 174
 DB 121 OGGHVAAGCGKKHKPKSAKKPAAAAA-----PASPERASSSVTSSMASSVAEEH 174
 QY 121 SSGREAAA-----PKKATKKAATAVAIDVPTTVSPSQSLSTTTT-----SAATTEBY 171
 DB 121 SSGREAAA-----PKKATKKAATAVAIDVPTTVSPSQSLSTTTT-----SAATTEBY 171
 QY 175 GNAGTSSASAVCAKESSFTSASEFOIDDSFWSFTLSMPLDGYVSM-----PGDAF 229
 DB 175 GNAGTSSASAVCAKESSFTSASEFOIDDSFWSFTLSMPLDGYVSM-----PGDAF 229
 QY 230 VAPPSA---DDM-DYWLGVFMESGEAODLPQI 257
 DB 227 GASPPSSNDMDPFLKLFIAQGMQNLPQI 258

RESULT 4

ADH50100
 ID ADH50100 standard; protein; 258 AA.

AC ADH50100;

DT 25-MAR-2004 (first entry)

DE Rice Myb-related transcription factor #1.

KW Myb-related transcription factor; transcriptional regulation; plant;
 gene regulation; rice.

OS Oryza sativa.

PN US2002187539-A1.

PD 12-DEC-2002.

PF 05-DEC-2001; 2001US-00008118.

PR 20-NOV-1998; 98US-0109294P.

PR 19-NOV-1999; 99US-00443704.

PA (CAHO/) CAHOON R E.

PA (WENG/) WENG Z.

PI Cahoon RE, Weng Z;

XX WPI; 2004-059062/06.
 DR N-PSDB; ADH50099.

XX A new isolated plant nucleic acid fragments encoding a Myb-related

PT transcription factor in plants and seeds, are useful to control gene

PT expression.

XX Claim 10; SEQ ID NO 4; 53pp; English.

XX The invention comprises the amino acid and coding sequences of Myb-
 CC related transcription factors - these proteins are involved in
 CC transcriptional regulation in plants. The DNA and protein sequences of
 CC the invention may be used to facilitate studies to better understand gene
 CC regulation in plants and provide genetic tools to enhance or otherwise
 CC alter the expression of genes controlled by Myb-related transcription
 CC factors. The present amino acid sequence represents an Myb-related
 CC transcription factor of the invention.

SO Sequence 258 AA;

Query Match 60.5%; Score 827.5; DB 8; Length 258;
 Best Local Similarity 62.1%; Pred. No. 2.3e-71;
 Matches 169; Conservative 29; Mismatches 45; Indels 29; Gaps 8;

QY 1 MGRAPCCCKMGLKKGWPTBEDKVLVAHIORHGNWRALPRQAGLLRCGKSCRLWIMY 60
 DB 1 MGRAPCCCKMGLKKGWPTBEDKVLVAHIORHGNWRALPRQAGLLRCGKSCRLWIMY 60
 QY 61 LRPDIRKGNFSEEDTIIHLHELGNRWSAIAARLPGRDNEIKVWHTLKKRLDAPA 120
 DB 61 LRPDIRKGNFSEEDTIIHLHELGNRWSAIAARLPGRDNEIKVWHTLKKRLDAPA 120
 QY 121 OGGHVAAGCGKKHKPKSAKKPAAAAA-----PASPERASSSVTSSMASSVAEEH 174
 DB 121 OGGHVAAGCGKKHKPKSAKKPAAAAA-----PASPERASSSVTSSMASSVAEEH 174
 QY 121 SSGREAAA-----PKKATKKAATAVAIDVPTTVSPSQSLSTTTT-----SAATTEBY 171
 DB 121 SSGREAAA-----PKKATKKAATAVAIDVPTTVSPSQSLSTTTT-----SAATTEBY 171
 QY 175 GNAGTSSASAVCAKESSFTSASEFOIDDSFWSFTLSMPLDGYVSM-----PGDAF 229
 DB 175 GNAGTSSASAVCAKESSFTSASEFOIDDSFWSFTLSMPLDGYVSM-----PGDAF 229
 QY 230 VAPPSA---DDM-DYWLGVFMESGEAODLPQI 257
 DB 227 GASPPSSNDMDPFLKLFIAQGMQNLPQI 258

RESULT 5

AAG54569
 ID AAG54569 standard; protein; 257 AA.

AC AAG54569;

DT 18-OCT-2000 (first entry)

DE Zea mays protein fragment SEQ ID NO: 69592.

KW Protein identification; signal transduction pathway; metabolic pathway;
 hybridisation assay; genetic mapping; gene expression control; promoter;
 termination sequence; corn.

OS Zea mays subsp. mays.

PN EP1033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-00301439.

PR 25-FEB-1999; 99US-0121825P.

PR 05-MAR-1999; 99US-0123180P.

PR 09-MAR-1999; 99US-0123548P.

PR 23-MAR-1999; 99US-0125788P.

PR 25-MAR-1999; 99US-0126264P.

PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 11-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
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PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139500P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-014091P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
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PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.

PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
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PR 20-JUL-1999; 99US-0144335P.
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PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
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PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
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PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
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PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145919P.
PR 02-AUG-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
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PR 04-AUG-1999; 99US-0147204P.
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PR 09-AUG-1999; 99US-0147493P.
PR 10-AUG-1999; 99US-0147935P.
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PR 11-AUG-1999; 99US-0148319P.
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PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153788P.
PR 15-SEP-1999; 99US-0154016P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0156589P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158023P.
PR 08-OCT-1999; 99US-0158232P.

PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
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PR 13-OCT-1999; 99US-0159295P.
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PR 14-OCT-1999; 99US-0159637P.
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PR 21-OCT-1999; 99US-0160741P.
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PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
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PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161820P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 58.4%; Score 799.5; DB 3; Length 257;

Best Local Similarity 58.8%; Pred. No. 1,2e-68; Matches 160; Conservative 30; Mismatches 51; Indels 31; Gaps 8;

QY 1 MGRAPCECEKGLKGPWTPEDDKVLVAHIOKHGKGNMRLPKQAGLRCKGKSLRMVY 60
DB 1 MGRSCECEKGLKGPWTPEDDKVLVAHIOKHGKGNMRLPKQAGLRCKGKSLRMVY 60
QY 61 LRPDIKGNFSGKEEDTIIHLHLLGNKWSAIAARLPRTDNEIKVWHHLKKRLD-AP 119
DB 61 LRPDIKGNFSGKEEDTIIHLHLLGNKWSAIAARLPRTDNEIKVWHHLKKRLD-AP 120
QY 120 AGCGHVAAGCKKKKKPKAKKPAALAAAP---PASPRSS--SSVTESSAASVAE 173
DB 121 AS---QQAARKRPYKKQOPPEPVYALKEPTGAVPVSPERSISTTTSTTADYSAAS 177
QY 174 HGNAGISASASVCAKESSFTSASEPQIDDSFMSSETISM--PLDGYVSMPCDA--- 228
DB 178 LENAG-----DSFTSEEDYQIDDSFMSSETLAMTTTVSFESGVQQAAGSFG 224
QY 229 -FVAPPSA--DDMDYVLGVFMESGEAODLPQI 257
DB 225 KSAAPPSSTNDMDFWLKLFMQASDQNLPOI 256

RESULT 6

AAG54568
ID AAG54568 standard; protein; 309 AA.

AC AAG54568;
XX

DT 18-OCT-2000 (first entry)
XX

DE Zee maye protein fragment SEQ ID NO: 69591.
XX

XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence; corn.

XX Zee maye subsp. maye.
OS

XX EPI03405-A2.
PN

XX

PD 06-SEP-2000.
XX 25-FEB-2000; 2000EP-00301439.
XX 25-FEB-1999; 99US-0121825P.
XX 05-MAR-1999; 99US-0123180P.
XX 09-MAR-1999; 99US-0123548P.
XX 23-MAR-1999; 99US-0125788P.
XX 25-MAR-1999; 99US-0126264P.
XX 29-MAR-1999; 99US-0127462P.
XX 01-APR-1999; 99US-0128234P.
XX 06-APR-1999; 99US-0128714P.
XX 08-APR-1999; 99US-0129845P.
XX 16-APR-1999; 99US-0130077P.
XX 19-APR-1999; 99US-0130449P.
XX 21-APR-1999; 99US-0130510P.
XX 23-APR-1999; 99US-0130891P.
XX 28-APR-1999; 99US-0131449P.
XX 30-APR-1999; 99US-0132048P.
XX 30-APR-1999; 99US-0132407P.
XX 04-MAY-1999; 99US-0132484P.
XX 05-MAY-1999; 99US-0132485P.
XX 06-MAY-1999; 99US-0132486P.
XX 06-MAY-1999; 99US-0132487P.
XX 07-MAY-1999; 99US-0132863P.
XX 11-MAY-1999; 99US-0134256P.
XX 14-MAY-1999; 99US-0134218P.
XX 14-MAY-1999; 99US-0134219P.
XX 14-MAY-1999; 99US-0134221P.
XX 18-MAY-1999; 99US-0134370P.
XX 19-MAY-1999; 99US-0134371P.
XX 20-MAY-1999; 99US-0135124P.
XX 21-MAY-1999; 99US-0135333P.
XX 24-MAY-1999; 99US-0135629P.
XX 25-MAY-1999; 99US-0136021P.
XX 27-MAY-1999; 99US-0136392P.
XX 28-MAY-1999; 99US-0136782P.
XX 01-JUN-1999; 99US-0137222P.
XX 03-JUN-1999; 99US-0137528P.
XX 04-JUN-1999; 99US-0137502P.
XX 07-JUN-1999; 99US-0137724P.
XX 08-JUN-1999; 99US-0138094P.
XX 10-JUN-1999; 99US-0138540P.
XX 10-JUN-1999; 99US-0138847P.
XX 14-JUN-1999; 99US-0139119P.
XX 16-JUN-1999; 99US-0139452P.
XX 16-JUN-1999; 99US-0139453P.
XX 17-JUN-1999; 99US-0139492P.
XX 18-JUN-1999; 99US-0139454P.
XX 18-JUN-1999; 99US-0139455P.
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XX 18-JUN-1999; 99US-0139463P.
XX 18-JUN-1999; 99US-0139750P.
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XX 21-JUN-1999; 99US-0139817P.
XX 22-JUN-1999; 99US-0139899P.
XX 23-JUN-1999; 99US-0140353P.
XX 23-JUN-1999; 99US-0140354P.
XX 24-JUN-1999; 99US-0140695P.
XX 26-JUN-1999; 99US-0140823P.
XX 29-JUN-1999; 99US-0140991P.
XX 30-JUN-1999; 99US-014187P.
XX 01-JUL-1999; 99US-0141842P.
XX 01-JUL-1999; 99US-0142154P.
XX 02-JUL-1999; 99US-0142055P.

PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142820P.
PR 12-JUL-1999; 99US-0142877P.
PR 13-JUL-1999; 99US-0143342P.
PR 14-JUL-1999; 99US-01433624P.
PR 15-JUL-1999; 99US-0144005P.
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PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144684P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
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PR 22-JUL-1999; 99US-0145192P.
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PR 27-JUL-1999; 99US-0145313P.
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PR 02-AUG-1999; 99US-0146386P.
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PR 03-AUG-1999; 99US-0146389P.
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PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
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PR 23-AUG-1999; 99US-0149802P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-015138P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154039P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.

PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158363P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
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PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 18-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160982P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161932P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 58.4%; Score 799.5; DB 3; Length 309;
Best Local Similarity 58.8%; Pred. No. 1,5e-68;
Matches 160; Conservative 30; Mismatches 51; Indels 31; Gaps 8;

QY 1 MGRAPCCCEMGILKKPMTPEEDKVLVAHIORHGNNWRALPKQAGILRCGKSCRUMINY 60
DB 53 MGRSPCCCEMGILKKPMTPEEDKVLVAHIORHGNNWRALPKQAGILRCGKSCRUMINY 112
QY 61 LRPDIKRGNFSEEDTIIHHELLGNFMSAIAARLPGRTDNEIKVWHTHLKKRLD-AP 119
DB 113 LRPDIKRGNFSEEDAIIOHQLGNFMSAIAARLPGRTDNEIKVWHTHLKKRLDAP 172
QY 120 AQCCHVAASGCKKHKPKSAKKPAAANAAP---PASPERAS--SVTESMSSVAE 173
DB 173 AS---QQAARKKPKKQPPVTLGPGTGAIVSPERSISTTTSTTADYSASS 229
QY 174 HGNAGISSASASVCAKESSFTSASEFOIDSFMSSETLSM--PLDGYDVSMEPGDA-- 228
DB 230 LENAG-----DSFTSEEDYQIDSFSESETLAMTTTYSFESSVQQAEGSG 276
QY 229 -FVAPPSA--DDMDYLVGVFMSGEAODLPQI 257
DB 277 KSAAPPSSSTNDMDFMKLTFMQASDMONLPQI 308

RESULT 7
ADA48106
ID ADA48106 standard; protein; 162 AA.
XX
AC ADA48106;
XX
DT 20-NOV-2003 (first entry)
XX
DE Rice protein conferring disease resistance in plants.

XX disease resistance; pathogen tolerance; plant pathogen; plant; rice.
XX
XX Oryza sativa.
XX
XX WO2003000906-A2.
XX
XX 03-JAN-2003.
XX
XX 21-JUN-2002; 2002WO-1B002453.
XX
XX 22-JUN-2001; 2001US-0300112P.
XX PR 26-SEP-2001; 2001US-0352277P.
XX PR 22-MAR-2002; 2002US-0366535P.
XX
XX (SYGN) SYNGENTA PARTICIPATIONS AG.
XX PA
XX Glazebrook J, Briggs S, Cooper B, Goff SA, Moughamer T;
XX Katagiri F, Kreps J, Provart N, Rieke D, Zhu T;
XX WPI; 2003-184052/18.
XX DR N-PSDB; ADA48105.
XX
XX New polynucleotide comprising a plant nucleotide sequence having an open
XX reading frame that encodes a polypeptide associated with disease
XX resistance, useful for conferring resistance or tolerance to a plant
XX pathogen.
XX
XX Claim 10; SEQ ID NO 176; 299PP; English.
XX
XX The invention relates to a novel isolated polynucleotide comprising a
XX plant nucleotide sequence having an open reading frame that encodes a
XX polypeptide associated with disease resistance or its fragment having
XX substantially the same activity as the full-length polypeptide. The
XX polynucleotide of the invention is useful for conferring resistance or
XX tolerance to a plant pathogen. The present sequence represents a gene
XX conferring disease resistance used in the invention.
XX
XX
SQ Sequence 162 AA;
Query Match 55.7%; Score 762.5; DB 6; Length 162;
Best Local Similarity 90.6%; Pred. No. 2.3e-65;
Matches 145; Conservative 2; Mismatches 8; Indels 5; Gaps 3;
QY 1 MGRAPCEKMGKKGWTEBEDKVLVAHIQRHGHGWRALPKQ-AGLRCGKSCRRLWIN 59
DB 1 MGRAPCEKMGKKGWTEBEDKVLVAHIQRHGHGWRALPKQAGLRCGKSCRRLWIN 60
QY 60 YLRPDIKRGNFSEEDDTIIHLHELLGN-RMSAIAARLPRTDNEIKVWHTLKKRLDA 118
DB 61 YLRPDIKRGNFSEEDDTIIHLHELLGNRMSAIAARFGRDNGIKVWHTLKKRLDA 120
QY 119 PAOGGHVAASGGKHKHKPKSAKPPAAAAA---PPASPER 155
DB 121 PAOGGHVAASGGKHKHKPKSAKPPAAAAADGRRRRPSPGPER 160
RESULT 8
ABM85964
ID ABM85964 standard; protein; 162 AA.
AC ABM85964;
XX
XX 02-JUN-2005 (first entry)
XX
XX Rice abiotic stress responsive polypeptide SEQ ID NO:4210.
XX DE
XX abiotic stress tolerance; transgenic plant; plant; cereal; agriculture.
XX KW
XX Oryza sativa.
XX OS
XX WO2003008540-A2.
XX PN
XX

PD 30-JAN-2003.
XX
XX 21-JUN-2002; 2002WO-US019668.
XX
XX 22-JUN-2001; 2001US-0300112P.
XX PR 24-AUG-2001; 2001US-0314662P.
XX PR 26-SEP-2001; 2001US-0325277P.
XX PR 21-NOV-2001; 2001US-0321232P.
XX
XX (SYGN) SYNGENTA PARTICIPATIONS AG.
XX PA
XX Kreps J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F;
XX Moughamer T, Provart N, Rieke D, Zhu T;
XX WPI; 2003-248011/24.
XX
XX New stress-responsive nucleic acid, useful for altering the
XX responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold
XX stress, salt stress or osmotic stress.
XX
XX Claim 1; SEQ ID NO 4210; 89PP; English.
XX
XX The invention relates to novel abiotic stress responsive polynucleotides
XX and polypeptides. Also disclosed are vectors, expression cassettes, host
XX cells, and plants containing such polynucleotides. Also disclosed are
XX methods for using the polynucleotides and polypeptides to alter the
XX responsiveness of a plant to abiotic stress. The invention is useful in
XX agriculture. The nucleic acid is useful for determining whether a test
XX plant has been exposed to an abiotic stress condition. It is also useful
XX for selecting an agent that alters abiotic stress regulated
XX polynucleotide expression in a plant cell, and to identify a homolog or
XX ortholog to an abiotic stress responsive polynucleotide. The nucleic acid
XX molecule and the polypeptide encoded by it are useful in altering the
XX responsiveness of a plant to an abiotic stress, such as cold stress, salt
XX stress, osmotic stress or any of their combinations. The present sequence
XX is used in the exemplification of the invention
XX
XX
SQ Sequence 162 AA;
Query Match 55.7%; Score 762.5; DB 7; Length 162;
Best Local Similarity 90.6%; Pred. No. 2.3e-65;
Matches 145; Conservative 2; Mismatches 8; Indels 5; Gaps 3;
QY 1 MGRAPCEKMGKKGWTEBEDKVLVAHIQRHGHGWRALPKQ-AGLRCGKSCRRLWIN 59
DB 1 MGRAPCEKMGKKGWTEBEDKVLVAHIQRHGHGWRALPKQAGLRCGKSCRRLWIN 60
QY 60 YLRPDIKRGNFSEEDDTIIHLHELLGN-RMSAIAARLPRTDNEIKVWHTLKKRLDA 118
DB 61 YLRPDIKRGNFSEEDDTIIHLHELLGNRMSAIAARFGRDNGIKVWHTLKKRLDA 120
QY 119 PAOGGHVAASGGKHKHKPKSAKPPAAAAA---PPASPER 155
DB 121 PAOGGHVAASGGKHKHKPKSAKPPAAAAADGRRRRPSPGPER 160
RESULT 9
AAG54570
ID AAG54570 standard; protein; 248 AA.
XX
XX AAG54570;
XX
XX 18-OCT-2000 (first entry)
XX
XX Zea mays protein fragment SEQ ID NO: 69593.
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
XX KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence; corn.
XX KW
XX Zea mays subsp. mays.
XX OS
XX EPI033405-A2.
XX PN
XX

XX 06-SEP-2000.
XX
PF 25-FEB-2000; 200SEP-00301433.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0122548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0131449P.
PR 28-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
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PR 04-MAY-1999; 99US-0132485P.
PR 05-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 14-JUN-1999; 99US-0138847P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140931P.
PR 30-JUN-1999; 99US-014187P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.

PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
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PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
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PR 19-JUL-1999; 99US-0144325P.
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PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
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PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
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PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147303P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.

Query Match 50.0%; Score 684; DB 8; Length 277;
 Best Local Similarity 48.2%; Pred. No. 2.1e-57;
 Matches 144; Conservative 37; Mismatches 52; Indels 66; Gaps 10;

QY 1 MGRAPCCCKGLKGPWTPPEEDKVLVAHIQRHGNWRALPKQAGLLRCGKSCRLRWINY 60
 |||||
 1 MGRAPCCCKGLKGPWTPPEEDKVLVAHIQRHGNWRALPKQAGLLRCGKSCRLRWINY 60

QY 61 LRPDIKRGNFSKEEDTIIHLHLLGNRMSAIAARLPRTDNEIKVWHTHLKKRLD--A 118
 |||||
 61 LRPDIKRGNFSKEEDTIIHLHLLGNRMSAIAARLPRTDNEIKVWHTHLKKRLD--A 118

QY 119 PAQGGHVAASGCKKKPKSAKPPAATAA-----PPASPRASAS 158
 |||||
 121 PPQ-----NPKRHSKNHDSKGPPTSSESSNNSHLTFITQKHIDSSVPAPSPQISS 173

QY 159 SSVTSSMASVAEHSNAGISSASASVCAKESSFTSASEEF-QIDDSFWSSETLSMP-- 215
 |||||
 174 -----TEMSTVTLV-DDH-----QWVIKQEE-MESSEYFPEIDESFTDLDXTDN 217

QY 216 -LDGYVSMPEGDA-----FVAPPSADDDMDYWLGVFMEGGEADLPQ 256
 :|||
 218 WENTHDVWVTAQDELQVLPFSSLKXENVMDLTTKEDDMDFMVNVFTKTDLPPELPE 276

Db 218 WENTHDVWVTAQDELQVLPFSSLKXENVMDLTTKEDDMDFMVNVFTKTDLPPELPE 276

RESULT 11
 AAW37811
 ID AAW37811 standard; protein; 278 AA.
 AC AAW37811;
 XX
 DT 17-OCT-2003 (revised)
 DT 17-AUG-1998 (first entry)

XX Tobacco Myb1 protein.
 DE Tobacco; Myb1 protein; transgenic plant; disease resistance.
 KM Nicotiana tabacum; cv. Xanthi nc.
 OS Nicotiana tabacum; cv. Xanthi nc.
 XX
 FH Key Location/Qualifiers
 FT Region /note= "imperfect tryptophan repeat"
 FT MISC-difference 53 /note= "conserved redox sensitive Cys"
 FT Region 65..115 /note= "imperfect tryptophan repeat"
 FT Region 179..278 /note= "acidic C-terminal region"

XX MO9813486-A1.
 PN
 XX
 XX 02-APR-1998.
 PD
 XX 26-SEP-1997; 97MO-US017415.
 PF
 XX 27-SEP-1996; 96US-00722626.
 PR
 XX (RUTP) UNIV RUTGERS STATE NEW JERSEY.
 PA
 XX Yang Y, Kleisig DF;
 PI
 XX WPI: 1998-230699/20.
 DR N-PSDB; AAV19105.
 XX
 XX Tobacco myb1 gene sequence - useful for, e.g. producing transgenic plants
 PT with improved disease resistance.
 XX
 XX Claim 17; Fig 1A; 66pp; English.
 PS
 XX This 32 kDa protein, designated Myb1, is the tobacco homologue of
 CC mammalian Myb and is involved in the regulation of disease resistance.

CC Its amino acid sequence was deduced from an isolated cDNA clone (see
 CC AAV19105). The encoded protein comprises a basic N-terminal region with 2
 CC imperfect tryptophan repeats, a potential ATP/GTP binding site or P-loop,
 CC a redox sensitive cysteine and a nuclear localisation sequence. The
 CC acidic C-terminal forms amphipathic alpha-helices which are
 CC characteristic of transcriptional activation domains. The Myb1 protein
 CC can be used to identify other proteins involved in both the
 CC hypersensitive and acquired disease resistant responses of plants, and
 CC also to raise Myb1-specific antibodies. The invention also provides novel
 CC transgenic plants, transformed with a vector including the myb1 gene,
 CC with enhanced disease resistance to certain pathogens. (updated on 17-OCT
 CC -2003 to standardise OS field)
 XX

SQ Sequence 278 AA;

Query Match 48.9%; Score 669.5; DB 2; Length 278;
 Best Local Similarity 47.2%; Pred. No. 5.2e-56;
 Matches 141; Conservative 37; Mismatches 56; Indels 65; Gaps 10;

QY 1 MGRAPCCCKGLKGPWTPPEEDKVLVAHIQRHGNWRALPKQAGLLRCGKSCRLRWINY 60
 |||||
 1 MGRAPCCCKGLKGPWTPPEEDKVLVAHIQRHGNWRALPKQAGLLRCGKSCRLRWINY 60

QY 61 LRPDIKRGNFSKEEDTIIHLHLLGNRMSAIAARLPRTDNEIKVWHTHLKKRLD--A 118
 |||||
 61 LRPDIKRGNFSKEEDTIIHLHLLGNRMSAIAARLPRTDNEIKVWHTHLKKRLD--A 118

QY 119 PAQGGHVAASGCKKKPKSAKPPAATAA-----PPASPRASAS 160
 |||||
 121 PPQ-----NSKRHSKNHDSKGPPTSSESSNNSDLTINTQKHIDSVLAPNSPQISS 173

QY 161 VTESMASVAEHSNAGISSASVCAKESSFTSASEEF-QIDDSFWSSETLS----- 213
 |||||
 174 STEMSTVTLV-DDH-----QWVIKQEE-VNESSEYFPEIDESFTDLDXTDNMS 221

QY 214 -----MPLDGYVSMPEGDAFVAPPSADDDMDYWLGVFMEGGEADLPQ 256
 :|||
 222 STDVHWVAAQDELQVLPFSSF---KEENVDLATKEDDMDFMVNVFTKTDLPPELPE 277

Db 222 STDVHWVAAQDELQVLPFSSF---KEENVDLATKEDDMDFMVNVFTKTDLPPELPE 277

RESULT 12
 AAG41251
 ID AAG41251 standard; protein; 285 AA.
 AC AAG41251;
 XX
 DT 18-OCT-2000 (first entry)
 DT
 XX Arabidopsis thaliana protein fragment SEQ ID NO: 51301.
 DE
 XX Protein identification; signal transduction pathway; metabolic pathway;
 KM hybridisation assay; genetic mapping; gene expression control; promoter;
 KM termination sequence.
 XX
 XX Arabidopsis thaliana.
 OS
 XX
 XX EP1033405-A2.
 PN
 XX 06-SEP-2000.
 PD
 XX 25-FEB-2000; 2000EP-00301439.
 PF
 XX 25-FEB-1999; 99US-0121825P.
 PR 05-MAR-1999; 99US-0123180P.
 PR 09-MAR-1999; 99US-0123548P.
 PR 23-MAR-1999; 99US-0125788P.
 PR 25-MAR-1999; 99US-0126264P.
 PR 29-MAR-1999; 99US-0126785P.
 PR 01-APR-1999; 99US-0127462P.
 PR 06-APR-1999; 99US-0128234P.
 PR 08-APR-1999; 99US-0128714P.
 PR 16-APR-1999; 99US-0128845P.
 PR 19-APR-1999; 99US-0130077P.

PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
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PR 05-MAY-1999; 99US-0132485P.
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PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
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PR 20-MAY-1999; 99US-0135124P.
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PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
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PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
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PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
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PR 18-JUN-1999; 99US-0139463P.
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PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
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PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
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PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.

PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144844P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
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PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
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PR 27-JUL-1999; 99US-0145918P.
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PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
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PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
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PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
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PR 26-AUG-1999; 99US-0150884P.
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PR 31-AUG-1999; 99US-0151438P.
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PR 07-SEP-1999; 99US-0152363P.
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PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
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PR 14-OCT-1999; 99US-0159330P.

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PR 21-OCT-1999; 99US-0160767P.
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PR 21-OCT-1999; 99US-0160815P.
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PR 22-OCT-1999; 99US-0160989P.
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PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161931P.
PR 29-OCT-1999; 99US-0162142P.
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Query Match 48.4%; Score 661.5; DB 3; Length 285;
Best Local Similarity 49.0%; Pred. No. 3.2e-55;
Matches 146; Conservative 25; Mismatches 66; Indels 61; Gaps 6;

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OY 1 MGRAPCCCKMGLKKGPMTPPEEDKVLVAH1QRHGNWRALPRQAGLLRCGKSCRLRWNY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 MGRAPCCCKMGLKKGPMTPPEEDKVLVSFLNHGSHWRALPRQAGLLRCGKSCRLRWNY 60
OY 61 LRPDIKRGNFSEEDTIIHLHLLGNRWSAIAALPRTDNEIKVWHTHLKKRLDAPA 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 LRPDIKRGNFTEEDDAIISLHQILGNRWSAIAAKLPRTDNEIKVWHTHLKKRLE-DY 119
OY 121 OGGHVAASGGKHKPKSAKKPAAAAAPASPERSASSSVSSWASSVAEHNAGIS 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 120 QPAKPKTSKKKGTTPKS-----ESVITSSNSTRESELAADS---SNPSGGS 163
OY 181 SASASVCAKESSFTSASEE-----FOJDSFWSFT 211
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 164 LFTSPSTSEVSMTLISHDGYSEINMDNKPQDITIDQECVSFETFGADIDESFWKET 223
OY 212 LSMPLDGYVS-----MERGDAFVAPPSAD-----DMDYVLGVFMESGEADL 254
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 224 LYSODEHNVNSDLVAGLVEIQOEFQNLGSANNEMIFDSEMDFWFDVLAFTGGEODL 281
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RESULT 13
ADN72611 standard; protein; 285 AA.

```
XX ADN72611;
XX
XX 15-JUL-2004 (first entry)
XX
XX Thale cress protein upregulated in E2Fa/Dpa expressing plants Segid 506.
XX
XX plant; transgenic; E2Fa/Dpa transcription factor; growth regulator;
XX animal feed product; thale cress; cell wall biosynthesis;
XX nitrogen metabolism; carbon metabolism.
XX
XX Arabidopsis thaliana.
XX
XX WO2004035798-A2.
XX
XX 29-APR-2004.
XX
XX 20-OCT-2003; 2003WO-EP011658.
XX
XX 18-OCT-2002; 2002EP-00079408.
XX
```

PA (CROP-) CROPEDESIGN NV.
XX Inze D, De Veylder L, Vlieghe K;
PI
XX WPI; 2004-348466/32.
DR N-PSDB; ADN72610.

PT Altering plant characteristic, useful for producing plants for enzyme or
PT pharmaceutical production comprises modifying in a plant, expression of
PT one or more nucleic acids and/or modifying level or activity of one or
PT more proteins.

PS Claim 1; SEQ ID NO 506; 134bp; English.

XX This invention relates to a novel method for altering one or more plant
XX characteristics. Specifically, it refers to identifying genes that are up
XX - or down-regulated in transgenic plants overexpressing the heterodimeric
XX E2Fa/Dpa transcription factor of Arabidopsis and using these sequences to
XX alter plant characteristics accordingly. The present invention describes
XX generating transgenic plants for the production of growth regulators,
XX enzymes, therapeutics, pharmaceuticals and animal feed products, where
XX the altered plant characteristics are selected from increased yield or
XX biomass, enhanced survival capacity, stress tolerance, plant architecture
XX or physiology, altered endoreduplication, biochemistry, signal
XX transduction, storage lipid mobilisation and/or altered photosynthesis,
XX each relative to the corresponding wild type plants. Accordingly, these
XX sequences can also be useful as positive or negative selectable markers
XX during transformation of cells or tissues. The identified genes play a
XX role in a variety of biological processes such as DNA replication, cell
XX wall biosynthesis, nitrogen and/or carbon metabolism or they function as
XX transcription factors. This polypeptide sequence is thale cress protein
XX expressed by a gene upregulated 1.3 fold or more in plants overexpressing
XX the E2Fa/Dpa transcription factor, given in an exemplification of the
XX invention.

XX Sequence 285 AA;

Query Match 48.4%; Score 661.5; DB 8; Length 285;
Best Local Similarity 49.0%; Pred. No. 3.2e-55;
Matches 146; Conservative 25; Mismatches 66; Indels 61; Gaps 6;

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OY 1 MGRAPCCCKMGLKKGPMTPPEEDKVLVAH1QRHGNWRALPRQAGLLRCGKSCRLRWNY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 MGRAPCCCKMGLKKGPMTPPEEDKVLVSFLNHGSHWRALPRQAGLLRCGKSCRLRWNY 60
OY 61 LRPDIKRGNFSEEDTIIHLHLLGNRWSAIAALPRTDNEIKVWHTHLKKRLDAPA 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 LRPDIKRGNFTEEDDAIISLHQILGNRWSAIAAKLPRTDNEIKVWHTHLKKRLE-DY 119
OY 121 OGGHVAASGGKHKPKSAKKPAAAAAPASPERSASSSVSSWASSVAEHNAGIS 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 120 QPAKPKTSKKKGTTPKS-----ESVITSSNSTRESELAADS---SNPSGGS 163
OY 181 SASASVCAKESSFTSASEE-----FOJDSFWSFT 211
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 164 LFTSPSTSEVSMTLISHDGYSEINMDNKPQDITIDQECVSFETFGADIDESFWKET 223
OY 212 LSMPLDGYVS-----MERGDAFVAPPSAD-----DMDYVLGVFMESGEADL 254
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 224 LYSODEHNVNSDLVAGLVEIQOEFQNLGSANNEMIFDSEMDFWFDVLAFTGGEODL 281
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RESULT 14
ADX91441 standard; protein; 304 AA.

```
XX ADX91441;
XX
XX 21-APR-2005 (first entry)
XX
XX Plant full length insert polypeptide segid 54105.
XX
XX plant protectant; plant growth regulant; gene therapy; plant;
```


KW	recombinant DNA construct; physical array; plant breeding marker;
KW	cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW	extreme osmotic condition; pathogen tolerance; pest tolerance;
KW	growth rate; cell cycle pathway; disease resistance;
KW	galactomannan production; lignin production; plant growth regulator;
KW	yield; plant growth; plant development; seed oil; protein yield;
KW	protein content.
XX	
OS	unidentified.
XX	
PN	US2004034888-A1.
XX	
PD	19-FEB-2004.
XX	
XX	28-APR-2003; 2003US-00425114.
PF	06-MAY-1999; 99US-00304517.
PR	05-NOV-2001; 2001US-00985678.
XX	
PA	(LIUJ/) LIU J.
PA	(ZHOU/) ZHOU Y.
PA	(KOVA/) KOVALIC D K.
PA	(SCRE/) SCREEN S E.
PA	(TABBA/) TABASKA J E.
PA	(CAOY/) CAO Y.
XX	
P1	Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
DR	WPI; 2004-180133/17.
XX	
PT	New recombinant DNA construct, useful for improving plant tolerance to
PT	cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT	pests, for conferring increased resistance to plant disease, or for
PT	improving yield.
XX	
PS	Claim 1; SEQ ID NO 54105; 15pp; English.
CC	The invention describes a recombinant DNA construct comprising a
CC	polynucleotide consisting of a sequence encoding an amino acid sequence
CC	available in electronic form from the US patent office at
CC	ftp.segdata.uspto.gov/sequence.html?docID:2004034888. The polynucleotide
CC	of the invention are also useful in physical arrays of molecules and as
CC	plant breeding markers. The recombinant DNA construct is useful for
CC	improving plant tolerance to cold, heat, drought, herbicides, extreme
CC	osmotic conditions, pathogens or pests, for manipulating growth rate in
CC	plant cells by modification of the cell cycle pathway, for conferring
CC	increased resistance to plant disease, for producing galactomannan,
CC	lignin or plant growth regulators, for increasing the rate of homologous
CC	recombination in plants, for improving yield by modification of
CC	photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC	or by providing improved plant growth and development under at least one
CC	stress condition or for modifying seed oil or protein yield and/or
CC	content. This is the amino acid sequence of a plant full length insert
CC	polypeptide that can be used in the recombinant DNA construct of the
CC	invention.
SQ	
SQ	Sequence 304 AA:
Query Match	48.4%; Score 661.5; DB 8; Length 304;
Best Local Similarity	49.0%; Pred. No. 3.6e-55;
Matches 146; Conservative 25; Mismatches 66; Indels 61; Gaps 5	
Db	1 MGRAPCCKMGLKKGPMTPEEDKVLVAHQHGGMNMLPPOAGLACGKSCLRWNY 60
20 MGRAPCCCKMGKRQPMPEEDQIVSTLNHGSHNMLPKQAGLTCGSCLRKNMY 79	
OY	LRPDIKGNFSKEEDITIIHLLELGNMSAIARLPRTDNEIRNVHTLKKRLDAPA 120
DB	80 LKPDIKGNFTKEEDAITLSHQILGNMWSAIAKLPGRTDNEIRNVHTLKKRLF-DY 138
OY	121 QCGHVAAAGCCKKHKKPKAKKRAAAAAAAPSPASPVSSSVTSSMASSVAEHNGNIS 180
DB	139 QPAKRTSNKKKGTRPKS-----ESVTSSNSTSESLAQS---SNPSES 182

Oy	181	SASASVCAKESSFTSASE-----FOIDSFMSFT 211
Dd	183	LFETSTSTSEVSMTLISHDGSNINMDKNRGDISTRIDCEVSFTFTGADIDBSFWKFT 242
Oy	212	LSMPLDGDYVS-----MEPGDAFVAPPSAD-----DMDYLVGFVMSGEAQL 254
Dd	243	LYSGDHNHYVNDLEVAGLVEIQGFQNLGSANNEMIFDSEMDPFWLARTGGEQL 300
RESULT 15		
ID	ADX71586	standard; protein; 313 AA.
XX	ADX71586;	
AC	ADX71586;	
XX		
DT	21-APR-2005	(first entry)
XX		
DE	Plant full length insert polypeptide seqid 40952.	
XX		
KM	plant protectant; plant growth regulant; gene therapy; plant;	
KM	recombinant DNA construct; physical array; plant breeding marker;	
KM	cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;	
KM	extreme osmotic condition; pathogen tolerance; pest tolerance;	
KM	growth rate; cell cycle pathway; disease resistance;	
KM	galactomannan production; lignin production; plant growth regulator;	
KM	plant growth; plant development; seed oil; protein yield;	
KM	protein content.	
XX		
OS	Unidentified.	
XX		
PN	US2004034888-A1.	
XX		
PD	19-FEB-2004.	
XX		
PF	28-APR-2003; 2003US-00425114.	
XX		
PR	06-MAY-1999; 99US-00304517.	
PR	05-NOV-2001; 2001US-00985678.	
XX		
PA	(LIU/)/ LIU J.	
PA	(ZHOU/)/ ZHOU Y.	
PA	(KOVA/)/ KOVALIC D K.	
PA	(SCRE/)/ SCREEN S E.	
PA	(TABAA/)/ TABASKA J E.	
PA	(CAOV/)/ CAO Y.	
XX		
P1	Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;	
XX		
DR	WPI; 2004-180133/17.	
XX		
PT	New recombinant DNA construct, useful for improving plant tolerance to	
PT	cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or	
PT	pests, for conferring increased resistance to plant disease, or for	
PT	improving yield.	
XX		
PS	Claim 1; SEQ ID NO 40952; 15pp; English.	
XX		
CC	The invention describes a recombinant DNA construct comprising a	
CC	polynucleotide consisting of a sequence encoding an amino acid sequence	
CC	available in electronic form from the US patent office at	
CC	ftp.segdata.uspto.gov/sequence.html?docID:2004034888. The polynucleotide	
CC	of the invention are also useful in physical arrays of molecules and as	
CC	plant breeding markers. The recombinant DNA construct is useful for	
CC	improving plant tolerance to cold, heat, drought, herbicides, extreme	
CC	osmotic conditions, pathogens or pests, for manipulating growth rate in	
CC	plant cells by modification of the cell cycle pathway, for conferring	
CC	increased resistance to plant disease, for producing galactomannan,	
CC	lignin or plant growth regulators, for increasing the rate of homologous	
CC	recombination in plants, for improving yield by modification of	
CC	photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake	
CC	or by providing improved plant growth and development under at least one	
CC	stress condition or for modifying seed oil or protein yield and/or	

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OM protein - protein search, using sw model

Run on: June 23, 2006, 23:59:07 ; Search time 41 Seconds
(without alignments)
603.115 Million cell updates/sec

Title: US-10-521-811-2

Perfect score: 1368

Sequence: 1 MGRAPCCCKMKGLKGPWTPB.....MDYVLGVFMESGEADLPQI 257

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Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1368	100.0	257	2	T03825	myb protein homolo
2	835.5	61.1	288	2	T05954	transcription fact
3	709.5	51.9	280	1	S26604	myb-related protei
4	697.5	51.0	276	2	T03823	probable myb-relat
5	687	50.2	265	2	T07395	myb-related transc
6	669.5	48.9	278	2	T03850	myb-related protei
7	628.5	45.9	246	2	D86197	hypothetical prote
8	623.5	45.6	246	1	S71283	myb-related protei
9	608	44.4	249	2	E84717	probable MYB fam1
10	582	42.5	122	1	S58294	myb-related protei
11	563.5	41.2	340	1	S04898	myb-related protei
12	562	41.1	274	2	D86300	hypothetical prote
13	550	40.2	368	2	T03828	myb protein - rice
14	546	39.9	299	2	T47917	probable transcrip
15	532	38.9	325	2	T51509	probable transcrip
16	529	38.7	296	2	A96603	probable Myb-fam1
17	527	38.5	376	2	T03988	Myb-like transcrip
18	525.5	38.4	421	1	S26605	myb-related protei
19	524.5	38.3	399	1	A36697	maize myb-related
20	517	37.8	326	2	T49966	myb-related protei
21	516.5	37.8	321	1	S45338	myb-related protei
22	513.5	37.5	323	2	T51621	myb-like protein f
23	512.5	37.5	324	2	B85064	MYB-like protein f
24	511.5	37.4	323	2	T51645	myb-related transc
25	509.5	37.2	239	2	T02984	myb-related protei
26	508.5	37.2	421	1	S24244	myb-related protei
27	508	37.1	365	2	D86470	F21H7.9 protein -
28	507.5	37.1	311	2	T03827	myb protein hemolo
29	507.5	37.1	330	2	F96775	hypothetical prote

30	506.5	37.0	327	2	T01038	myb-related protei
31	505.5	37.0	282	2	B85327	probable transcrip
32	505.5	37.0	332	1	S58283	myb-related protei
33	505	36.9	343	2	T48050	probable transcrip
34	505	36.9	352	1	S58293	myb-related protei
35	500	36.5	453	2	T09745	myb-related protei
36	499.5	36.5	36	1	J00956	myb-related protei
37	498	36.4	276	2	T02985	myb-related protei
38	497	36.3	294	2	T09879	myb-related protei
39	495.5	36.2	282	2	T05690	myb-related transc
40	495.5	36.2	333	2	T45720	probable transcrip
41	494.5	36.1	282	2	T51632	myb-related transc
42	493.5	36.1	251	1	S35729	myb-related protei
43	490	35.8	274	1	J00957	myb-related protei
44	489.5	35.8	255	1	S04899	myb-related protei
45	489	35.7	347	2	T07398	myb-related transc

ALIGNMENTS

RESULT 1

T03825 myb protein homolog - rice

C/Species: Oryza sativa (rice)

C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 31-Dec-2004

C/Accession: T03825

R/Coraggio, I.

submitted to the EMBL Data Library, February 1997

A/Reference number: Z15103

A/Accession: T03825

A/Status: preliminary; translated from GB/EMBL/DDB1

A/Molecule type: mRNA

A/Residues: 1-257 <COR>

A/Cross-references: UNIPROT:O04140; UNIPARC:UP100000ACEBA; EMBL.Y11414; PIDN:CAA72217.1

A/Experimental source: cv. Arborio, coleoptile

C/Genetics:

A/Gene: myb

C/Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology

F/9-61/Domain: myb DNA-binding repeat homology <MYB1>

F/62-112/Domain: myb DNA-binding repeat homology <MYB>

Query Match Best Local Similarity 100.0%; Score 1368; DB 2; Length 257;

Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MGRAPCCCKMKGLKGPWTPBEDKVLVAHIQRHGNWRALPKQAGLLRCGSKRLRWINY	60
Db	1	MGRAPCCCKMKGLKGPWTPBEDKVLVAHIQRHGNWRALPKQAGLLRCGSKRLRWINY	60
Qy	61	LRPDIKGNFSKEEDTTIHLHLLGNRSALAAALPGRDNEIKVMMHLLKKRLDAPA	120
Db	61	LRPDIKGNFSKEEDTTIHLHLLGNRSALAAALPGRDNEIKVMMHLLKKRLDAPA	120
Qy	121	QGGHVAASGGKKKKPKSAKPPAAAAAPPASPERASASSVTSSMASSVAEEHGNAGIS	180
Db	121	QGGHVAASGGKKKKPKSAKPPAAAAAPPASPERASASSVTSSMASSVAEEHGNAGIS	180
Qy	181	SASASVCAREESSFTSASEFOIDSFWSETTSLMPLDGVSNPQDAFVAPPADMDY	240
Db	181	SASASVCAREESSFTSASEFOIDSFWSETTSLMPLDGVSNPQDAFVAPPADMDY	240
Qy	241	WLGVMESGEADLPQI 257	
Db	241	WLGVMESGEADLPQI 257	

RESULT 2

T05954 transcription factor myb4 - barley (fragment)

C/Species: Hordeum vulgare (barley)

C/Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 31-Dec-2004

C/Accession: T05954

A/Cross-references: UNIPROT:Q04174; UNIPARC:UPI00000A5618; EMBL:X98308; NID:G1370139; P1
 A/Experimental source: cultivar Ailsa Craig; hypocotyl
 C/Genetics:
 A/Gene: THM18
 C/Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology
 C/Keywords: DNA binding; transcription regulation
 F/9-61/Domain: myb DNA-binding repeat homology <MYB1>
 F/62-112/Domain: myb DNA-binding repeat homology <MYB>

Query Match 50.2%; Score 687; DB 2; Length 265;
 Best Local Similarity 50.7%; Pred. No. 8.1e-44;
 Matches 143; Conservative 38; Mismatches 57; Indels 44; Gaps 9;

QY 1 MGRAPCCCKMGLKGGWTPBEDKVLVAHIOHGHGWRALPKOAGLLRCKGSKRLRWNY 60
 DB 1 MGRAPCCCKMGLKGGWTPBEDKVLVAHIOHGHGWRALPKOAGLLRCKGSKRLRWNY 60
 QY 61 LRPDIKRGNFTKEEDDTIILHLLGNRWSAIAARLPGRDNEIKVWHTLKKRLDAPA 120
 DB 61 LRPDIKRGNFTKEEDDTIILHLLGNRWSAIAARLPGRDNEIKVWHTLKKRLDAPA 120
 QY 121 OGCHVAASGKGGKHKKK--SAKKPAAAAA-----PPASPERASSSVTE 163
 DB 118 --NYPCQNSKRSKTSKSHVSNKGPPTSSESNNSDLSTSTKQIKIAPNSPOLSSS----E 171
 QY 164 SSMASVAEHEHGNAGISSASVCAKEESFTSASEF-QIDSPFMSSETLSMP---LDGY 219
 DB 172 MSSTVLIVDD-----NQWYIKEEKTESSSSSEYFKIDSFMADELSTENNMIIIGH 222
 QY 220 D-----VSMERGDAP-VAPPSADMDYVLGVFMESGEAODLPQ 256
 DB 223 DGEIGVEENVDIFTTSSKMEEDMDPMVNVFIRTKGLPELPE 264

RESULT 6

myb-related protein myb1, TMV-inducible - common tobacco
 T03850
 C/Species: Nicotiana tabacum (common tobacco)
 C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 31-Dec-2004
 C/Accession: T03850
 R/Yang, Y.; Kleesig, D.F.
 Proc. Natl. Acad. Sci. U.S.A. 93, 14972-14977, 1996
 A/Title: Isolation and characterization of a tobacco mosaic virus-inducible myb oncogene
 A/Reference number: Z15119; MUID:97121500; PMID:8962166
 A/Accession: T03850
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-278 <YAN>
 A/Cross-references: UNIPROT:P93391; UNIPARC:UPI000009F9F2; EMBL:U72762; NID:G1732246; P1
 A/Experimental source: strain Xanthi nc
 C/Genetics:
 A/Gene: myb1
 C/Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology
 C/Keywords: DNA binding; transcription regulation
 F/9-61/Domain: myb DNA-binding repeat homology <MYB1>
 F/62-112/Domain: myb DNA-binding repeat homology <MYB>

Query Match 48.9%; Score 669.5; DB 2; Length 278;
 Best Local Similarity 47.2%; Pred. No. 1.7e-42;
 Matches 141; Conservative 37; Mismatches 56; Indels 65; Gaps 10;

QY 1 MGRAPCCCKMGLKGGWTPBEDKVLVAHIOHGHGWRALPKOAGLLRCKGSKRLRWNY 60
 DB 1 MGRAPCCCKMGLKGGWTPBEDKVLVAHIOHGHGWRALPKOAGLLRCKGSKRLRWNY 60
 QY 61 LRPDIKRGNFTKEEDDTIILHLLGNRWSAIAARLPGRDNEIKVWHTLKKRLDAPA 118
 DB 61 LRPDIKRGNFTKEEDDTIILHLLGNRWSAIAARLPGRDNEIKVWHTLKKRLDAPA 120
 QY 119 PAOGCHVAASGKGGKHKKK--AKKPAAAAA-----APPASPERASSS 160
 DB 121 PQO-----NSKRHSKSNKHSKGPSTSSSNNSDLTIINTQKIDSPVLAENSPQISS 173

QY 161 VTSSMASVAEHEHGNAGISSASVCAKEESFTSASEF-QIDSPFMSSETLS----- 213
 DB 174 STEMSTVTLV-DH-----QMVIKOE--VMESSEVFPEIDSEFWDELDTNNMS 221
 QY 214 -----MPLDGYVSMERGDAPVAPPSADMDYVLGVFMESGEAODLPQ 256
 DB 222 STDHVVAAANQELQVLPFESSF---KEENVDIATKMEEDMDPMVNVFIRTKGLPELPE 277

RESULT 7

hypoetical protein [imported] - Arabidopsis thaliana
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2004
 C/Accession: D86197
 R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso
 Chin, C.W.; Chung, M.K.; Com, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.
 Nature 408, 816-820, 2000
 A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Malt, R.; Marziani
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon,
 Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A/Reference number: A86141; MUID:21016719; PMID:11130712
 A/Accession: D86197
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-246 <STO>
 A/Cross-references: UNIPROT:Q9LNC9; UNIPARC:UPI00000A8D57; GB:A8005172; NID:G8844123; P
 C/Genetics:
 A/Map position: 1
 C/Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology

Query Match 45.9%; Score 628.5; DB 2; Length 246;
 Best Local Similarity 48.0%; Pred. No. 1.6e-39;
 Matches 132; Conservative 35; Mismatches 59; Indels 49; Gaps 8;

QY 1 MGRAPCCCKMGLKGGWTPBEDKVLVAHIOHGHGWRALPKOAGLLRCKGSKRLRWNY 60
 DB 1 MGRAPCCCKMGLKGGWTPBEDKVLVAHIOHGHGWRALPKOAGLLRCKGSKRLRWNY 60
 QY 61 LRPDIKRGNFTKEEDDTIILHLLGNRWSAIAARLPGRDNEIKVWHTLKKRLDAPA 120
 DB 61 LRPDIKRGNFTKEEDDTIILHLLGNRWSAIAARLPGRDNEIKVWHTLKKRLDAPA 116
 QY 121 OGCHVAASGKGGKHKKKAKKP--AAAAAPASPERASSSVTSSMASVAEHEHGNAG 178
 DB 117 -----HSGQONNKEDPVSSTTAEMPTSPQOQSSSAD-----ISAITLGNND 161
 QY 179 ISSASASVCAKEESFTSASEFQ-IDSPFMSSETLSMPD-----GYDVSMER 225
 DB 162 ISNS-----KDSATSEEDVLAIIIDSEFWSEVLMDCDISGENEKKIEWEGSLDR 214
 QY 226 GDAFVAPPSADMDYVLGVFMES---GEAODLPQ 256
 DB 215 ND-----KGYNHDMFHFHLLTSSCTIGMSDISE 245

RESULT 8

myb-related protein, 28K, leaf-specific - Arabidopsis thaliana
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change 31-Dec-2004
 C/Accession: S71283
 R/Kirik, V.; Koelle, K.; Misera, S.; Baumlein, H.
 A/Description: The expression of a new leaf-specific myb gene is shifted to late embryo
 A/Reference number: S71283
 A/Accession: S71283
 A/Molecule type: DNA
 A/Residues: 1-246 <KIR>

A:Cross-references: UNIPROT:Q39153; UNIPARC:UPI00000A0F29; EMBL:Z50869; NID:G1263092; P1
A:Experimental source: strain Columbia
C:Genetics:
A:Introns: 45/1; 88/2
C:Superfamily: Myb-DNA-related transcription activator; myb DNA-binding repeat homology
C:Keywords: DNA binding; duplication; nucleus; transcription regulation
F:9-61/Domain: myb DNA-binding repeat homology <MYB1>
F:62-112/Domain: myb DNA-binding repeat homology <MYB2>

Query Match 45.6%; Score 623.5; DB 1; Length 246;
Best Local Similarity 47.3%; Pred. No. 3,8e-39;
Matches 130; Conservative 37; Mismatches 59; Indels 49; Gaps 8;

QY 1 MGRAPCCCKMGLKKGWTPPEEDKVLVAHIQRHGHGWMRALPKQAGLLRCGSKRLRWINY 60
DB 1 MGRAPCCCKMGLKKGWTPPEEDKVLVAHIQRHGHGWMRALPKQAGLLRCGSKRLRWINY 60
QY 61 LRPDIKRGNFSEEDTIIHLHELGNRWSAIAARLPGRTDNEIKVWHTHLKKRLDAPA 120
DB 61 LRPDIKRGNFSEEDTIIHLHELGNRWSAIAARLPGRTDNEIKVWHTHLKKRLDAPA 120
QY 121 OGCHVAASGKKHKKPKSAKKP-AAAAAPASPERSASSSVTSSMASSVAEEHGNAG 178
DB 61 LRPDIKRGNFSEEDTIIHLHELGNRWSAIAARLPGRTDNEIKVWHTHLKKRLDAPA 116
QY 117 -----HHSQDNKKEDFVSTTAEMPTSPQOQSSASAD-----ISATTTGANNND 161
DB -----HHSQDNKKEDFVSTTAEMPTSPQOQSSASAD-----ISATTTGANNND 161
QY 179 ISSASAVCAKESSFTSASEFQ-IDDSFVSETL-----SMPLDGYDVMSP 225
DB 162 INSN-----KDSATSSSEDLATIDBSFSEVLTDCDISGNEKEKKEIENWBSLDR 214
QY 226 GDAFVAPFADMDVYLGVFMES---GGAODLPQ 256
DB 215 ND-----KGYNDMEFWFDHLTSSSCITIGMSDISE 245

RESULT 9

884717
probable MYB family transcription factor [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 31-Dec-2004
C:Accession: E84717
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffatt, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Niernan, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: E84717
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-249 <STO>
A:Cross-references: UNIPROT:Q9SUX8; UNIPARC:UPI00000A5AF4; GB:A5002093; NID:G4432813; P1
A:Gene: At2G31180
A:Map position: 2
C:Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology

Query Match 44.4%; Score 608; DB 2; Length 249;
Best Local Similarity 43.3%; Pred. No. 5,4e-38;
Matches 122; Conservative 38; Mismatches 62; Indels 60; Gaps 5;

QY 1 MGRAPCCCKMGLKKGWTPPEEDKVLVAHIQRHGHGWMRALPKQAGLLRCGSKRLRWINY 60
DB 1 MGRAPCCCKMGLKKGWTPPEEDKVLVAHIQRHGHGWMRALPKQAGLLRCGSKRLRWINY 60
QY 61 LRPDIKRGNFSEEDTIIHLHELGNRWSAIAARLPGRTDNEIKVWHTHLKKRLDAPA 120
DB 61 LRPDIKRGNFSEEDTIIHLHELGNRWSAIAARLPGRTDNEIKVWHTHLKKRLDAPA 120
QY 121 OGCHVAASGKKHKKPKSAKKPAAAAAPASPERSASSSVTSSMASSVAEEHGNAGS 180
DB 121 NNG-----GDKVDVNGINNETTNEEDKGSIVYD 146
QY 181 SASASVCAKESSFTSASEFQ-----IDDSFVSETLSP-LDGYDVSMEPGA 228

DB 147 TASLQFNSITTFPIISNDKODIMSIEDISALIDSFSDVISTVDSNKNKEKIEDWEG 206
QY 229 EVAPPSA-----DDNDYVLGVFMES---GGAODLPQ 256
DB 207 LIDRNSKCKSYNSKLYNDMDMEFVFTSNRIEFSIDPE 248

RESULT 10

S58294
myb-related protein Y19 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 14-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C:Accession: S58294
R:Quaedvlieg, N.E.M.; Dockx, J.; Keultjes, G.G.M.; Sneekens, J.C.M.
submitted to the EMBL Data Library, July 1995
A:Reference number: S58280
A:Accession: S58294
A:Molecule type: DNA
A:Residues: 1-132 <OUA>
A:Cross-references: UNIPROT:Q39260; UNIPARC:UPI000009FC92; EMBL:X90384; NID:G928966; P1
C:Genetics:
A:Introns: 44/3; 88/3
C:Superfamily: Arabidopsis myb-related protein Y19; myb DNA-binding repeat homology
C:Keywords: DNA binding; duplication; nucleus; transcription regulation
F:9-61/Domain: myb DNA-binding repeat homology <MYB1>
F:62-112/Domain: myb DNA-binding repeat homology <MYB2>

Query Match 42.5%; Score 582; DB 1; Length 122;
Best Local Similarity 85.5%; Pred. No. 2e-36;
Matches 100; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

QY 1 MGRAPCCCKMGLKKGWTPPEEDKVLVAHIQRHGHGWMRALPKQAGLLRCGSKRLRWINY 60
DB 1 MGRAPCCCKMGLKKGWTPPEEDKVLVAHIQRHGHGWMRALPKQAGLLRCGSKRLRWINY 60
QY 61 LRPDIKRGNFSEEDTIIHLHELGNRWSAIAARLPGRTDNEIKVWHTHLKKRLD 117
DB 61 LRPDIKRGNFSEEDTIIHLHELGNRWSAIAARLPGRTDNEIKVWHTHLKKRLD 117

RESULT 11

S04898
myb-related protein 1 - maize
N:Alternate names: myb-related protein Zml
C:Species: Zea mays (maize)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 31-Dec-2004
C:Accession: S04898
R:Marocco, A.; Wiesenbach, M.; Becker, D.; Paz-Ares, J.; Siedler, H.; Salami, F.; Roh
Mol. Gen. Genet. 216, 183-187, 1989
A:Title: Multiple genes are transcribed in Hordeum vulgare and Zea mays that carry the
A:Reference number: S04896; MUID:89313655; PMID:2664447
A:Accession: S04898
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-340 <MAR>
A:Cross-references: UNIPROT:P20024; UNIPARC:UPI000012FAD8
C:Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology
C:Keywords: DNA binding; duplication; nucleus; transcription regulation
F:11-63/Domain: myb DNA-binding repeat homology <MYB1>
F:64-114/Domain: myb DNA-binding repeat homology <MYB2>

Query Match 41.2%; Score 563.5; DB 1; Length 340;
Best Local Similarity 49.4%; Pred. No. 1,6e-34;
Matches 118; Conservative 26; Mismatches 50; Indels 45; Gaps 6;

QY 2 GRAPCCCKMGLKKGWTPPEEDKVLVAHIQRHGHGWMRALPKQAGLLRCGSKRLRWINY 61
DB 4 GRAPCCAKVGLRGWSWTPPEEDKRLVAYIQKHGHTNRALPKQAGLLRCGSKRLRWINY 63
QY 62 RPDIKRGNFSEEDTIIHLHELGNRWSAIAARLPGRTDNEIKVWHTHLKKRLDAPA 121
DB 64 RPDIKRGNFSEEDTIIHLHELGNRWSAIAARLPGRTDNEIKVWHTHLKKRV----- 118

QY 122 GGHVAASGGKKKKPKSAKPPAAAAAPPASPERSSSVT--ESSMASSVAEHNAGI 179
 A:Residues: 1-368 <COR>
 A:Cross-references: UNIPROT:O04141; UNIPARC:UP100000A0C830; EMBL:Y11415; P1DN:CAA72218.1
 A:Experimental source: cv. Arduo, coleoptile
 C:Genetics:
 A:Gene: myb
 C:Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology
 F:62-112/Jomatin: myb DNA-binding repeat homology <MYB>

DB 119 -----AQREKKKAGSGSDAGTPATAPLSSATSTTTNNGSGSSGQCCGTSRP 168
 180 SASASVCARESSFTSASEEFOIDDSFMSSETLMPDGYDVMEPGDAFVAPPADDM 238
 169 PPAAT-DVC-----TLQPEDMDVSD-----MLVDG-----APPAQPM 199

RESULT 12
 D86300
 hypothetical protein F309.29[imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #ext_change 31-Dec-2004
 C:Accession: D86300
 R:Theologis, A.; Eckert, J.R.; Palm, C.J.; Federpiet, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 Ansen, N.F.; Hughes, B.; Hultzer, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopeon, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon,
 Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; M0ID:21016719; PMID:1110712
 A:Accession: D86300
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-274 <STO>
 A:Cross-references: UNIPROT:Q9SA47; UNIPARC:UP100000D685; GB:AE005172; NID:94966369; P1
 C:Genetics:
 A:Map position: 1
 C:Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology

Query Match 41.1%; Score 562; DB 2; Length 274;
 Best Local Similarity 45.4%; Pred. No. 1.6e-34;
 Matches 114; Conservative 36; Mismatches 67; Indels 34; Gaps 6;

QY 2 GRAPCCCKMGLKGPWTPEEDKVLVAHIORHGNMRLPKQAGLRCGKSCRLRWNY 61
 4 GRAPCCCKMGLKGPWTPEEDKVLVAHIORHGNMRLPKQAGLRCGKSCRLRWNY 63
 DB 62 RPDYKRGNFSEEDTTHLHLLGNRMAIARLPGRTDNEIKVWHTLKKRLDPAQ 121
 64 RPDYKRGNFSEEDTTHLHLLGNRMAIARLPGRTDNEIKVWHTLKKRLDPAQ 123
 DB 122 -GGHVAASGGKKKKPKSAKPPAAAAAPPASPERSSSVTSSMASSVAEHNAGIS 180
 124 LNADKSGKSLNEENSOE-----SSPNAKMSFA-----GSNISKDDDAQIS 167
 QY 181 SASASVCARESSFTSASEE-----FOIDDSFMSSETLMPDGYDVMEPGDAFV 230
 169 QMFEHLTVSE--FTQMLEVQKPELLEMPFDLPPIWSE--IDGSDSFQGPENRAL 220
 DB 231 APPSADMDY 241
 DB 221 QSESEDEVK 231

RESULT 13
 T03828
 myb protein - rice
 C:Species: Oryza sativa (rice)
 C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #ext_change 31-Dec-2004
 C:Accession: T03828
 R:Coraggio, I.
 Submitted to the EMBL Data Library, February 1997
 A:Reference number: Z15103
 A:Accession: T03828
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA

A:Residues: 1-368 <COR>
 A:Cross-references: UNIPROT:O04141; UNIPARC:UP100000A0C830; EMBL:Y11415; P1DN:CAA72218.1
 A:Experimental source: cv. Arduo, coleoptile
 C:Genetics:
 A:Gene: myb
 C:Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology
 F:62-112/Jomatin: myb DNA-binding repeat homology <MYB>

Query Match 40.2%; Score 550; DB 2; Length 368;
 Best Local Similarity 41.0%; Pred. No. 1.7e-33;
 Matches 129; Conservative 35; Mismatches 75; Indels 76; Gaps 10;

QY 1 MGRAPCCCKMGLKGPWTPEEDKVLVAHIORHGNMRLPKQAGLRCGKSCRLRWNY 60
 DB 1 MGRAPCCCKMGLKGPWTPEEDKVLVAHIORHGNMRLPKQAGLRCGKSCRLRWNY 60
 QY 61 LRPDYKRGNFSEEDTTHLHLLGNRMAIARLPGRTDNEIKVWHTLKKRLDPAQ 116
 DB 61 LRPDYKRGNFSEEDTTHLHLLGNRMAIARLPGRTDNEIKVWHTLKKRLDPAQ 120
 QY 117 -DAPACGGHVAASGGKKKKPK-----SAKPPAAAAAPPASPE----- 154
 DB 121 IDPVTFA-----PRDLIDLTLKLPAAAAAYYPQADLDLRLALEPLAGYP 167
 QY 155 ---RSASS---SVTSSMASSVAEHNAGISSASASVCARESSFT-----SASE 199
 DB 168 DLRLASALPLPAITTTGAAAAAABOAFPLMLQAQMAQOQQQVTPPPPPPPQAAAT 227
 QY 200 EFOIDDSFMSSETLMPDGYDVMEPGDAFVAP-----PSADD-MDY 241
 DB 228 QFLQATRS-----TCHQMPGLVHASPQQLAQOQDHMAAATCRAGAVQHPVDNQLDY 283
 QY 242 LGVFMESGEAQLDLP 256
 DB 284 PALMQMASDASNLQ 298

RESULT 14

T47917
 probable transcription factor MYB17 - Arabidopsis thaliana
 N:Alternate names: protein T20K12.150
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #ext_change 31-Dec-2004

C:Accession: T47917; T51638
 R:Kranz, H.D.; Denekamp, M.; Greco, R.; Jin, H.; Kranz, H.D.; Denekamp, M.; Greco, R.;
 Paz-Ares, J.; Welsch, B.
 Plant J. 16, 263-276, 1998
 A:Title: Towards functional characterisation of the members of the R2R3-MYB gene from A
 A:Reference number: Z14349; M0ID:9839469; PMID:9839469
 A:Accession: T47917

A:Molecule type: DNA
 A:Residues: 1-299 <DB>
 A:Cross-references: UNIPROT:Q9M2D9; UNIPARC:UP100000A65F8; EMBL:AL137898
 A:Experimental source: cultivar Columbia; BAC clone T20K12
 R:Kranz, H.D.; Denekamp, M.; Greco, R.; Jin, H.; Kranz, H.D.; Denekamp, M.; Greco, R.;
 Paz-Ares, J.; Welsch, B.
 Plant J. 16, 263-276, 1998
 A:Title: Towards functional characterisation of the members of the R2R3-MYB gene from A
 A:Reference number: Z14349; M0ID:9839469; PMID:9839469
 A:Accession: T51638
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 76-116, 'Y', 118-299 <RA>
 A:Cross-references: UNIPARC:UP100000A0A8B8; EMBL:AF062866; P1DN:AA03508.1
 A:Experimental source: cultivar Columbia
 C:Genetics:
 A:Gene: MYB17
 A:Map position: 3
 A:Introns: 45/1; 88/2
 A>Note: T20K12.150
 C:Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology

Query Match 39.9%; Score 546; DB 2; Length 299;
 Best Local Similarity 43.4%; Pred. No. 2.7e-33;
 Matches 121; Conservative 35; Mismatches 81; Indels 42; Gaps 5;

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QY 1 MGRAPCCCEKMGILKKGPWTPBEDKVLVAHIQRHGHGNWRALPKQAGLLRCGKSCRLRWINY 60
DB 1 MGRTPCCDCKIGLKKGPWTPBEDKVLVAHIKKNGHGSWRTLPKLAGLLRCGKSCRLRWINY 60
QY 61 LRPDIKRGNFSKEEDPTIHLHELGNRWSAIAARLPGRDNEIKVWHTHLKKRL---D 117
DB 61 LRPDIKRGNFSKEEDPTIHLHELGNRWSAIAARLPGRDNEIKVWHTHLKKRLLSMG 120
QY 118 APAQGHVAASGGKGGKPKKSAKPPAAAAAPAPSPERSASSVTESSMASSVAEEHG-- 175
DB 121 LDPRTHEPLPSYGLAKQAPSS---PTTRHMAQWESARVAEARLSRESMLFSPSPYSGVV 177
QY 176 -----NAGISSASAVCAKESSFTSASEEFOI-----DDSPMSETLS 213
DB 178 KTECHFLRIWNSSEIGEAFFRNLAFLDESTITTSQSPCSRATSTSSALLKSTNSWGGEVY 237
QY 214 MPIDGYDVSMPEPD-----AFVAPSPADMDY 240
DB 238 VAHGSDDYSPYGNLDEDDSTDSALQLLDFPISDDMSF 276
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RESULT 15

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T51509
probable transcription factor (MYB9) - Arabidopsis thaliana
N:Alternate names: protein F5E19_110
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 31-Dec-2004
C:Accession: T51509
R:Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.; Mew
submitted to the Protein Sequence Database, August 2000
A:Reference number: Z25394
A:Accession: T51509
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-325 <SAT>
A:Cross-references: UNIPROT:Q9LFE1; UNIPARC:UP100000AA6D3; EMBL:AL391147
A:Experimental source: cultivar Columbia; BAC clone F5E19
C:Genetics:
A:Map position: 5
A:Introns: 88/2
A>Note: F5E19_110
C:Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology
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Query Match 38.9%; Score 532; DB 2; Length 325;

Best Local Similarity 44.3%; Pred. No. 3.2e-32; Mismatches 66; Indels 48; Gaps 7;

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DB 1 MGRAPCCCEKMGILKKGPWTPBEDKVLVAHIQRHGHGNWRALPKQAGLLRCGKSCRLRWINY 60
1 MGRSPCCDCKIGLKKGPWTPBEDKVLVAHIKKNGHGSWRTLPKLAGLLRCGKSCRLRWINY 60
QY 61 LRPDIKRGNFSKEEDPTIHLHELGNRWSAIAARLPGRDNEIKVWHTHLKKRLDAPA 120
DB 61 LRPDIKRGNFSKEEDPTIHLHELGNRWSAIAARLPGRDNEIKVWHTHLKKRL---L 117
QY 121 QGHVAASGGKGGKPKKSAKPPAAAAAPAPSPERSASSVTESSMASSVAEEHG-- 152
DB 118 QMGIDPVT---HRPRTHLNVLAALPQIIAANFNLSLNLNQNVOLDATTAKAQLH 172
QY 153 ---PERSASSVTESSMASSVAEEHGNAGISSASAVCAKESSFTSASEEFO---IDS 206
DB 173 TMIQVLTNNNTNTPSPSSSTMQNSNTNLFQAS---YIENQNLFGQSGNFSHILEDEN 228
QY 207 FWSSET--LSMPLDGYDVSMPEG 226
DB 229 LMVKTQIIDNPLDPSFSSPIQPG 250
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Search completed: June 24, 2006, 00:04:35
Job time : 42 secs

Oy	317	ATCTCCAGAGTGGCTGGGCAACAGTGGTCCGCAATTCCCGCAGGTGGCCCGGAGGA	376
Db	491	GCCTCCACAACCTCCCTCGGCAACAGGTGGTCAGCATTCCCGCCAGATGCCGGGTGCA	550
Oy	377	CGSACAAGAGATCAAGAACGTGTGGCACCCACCTCAAGAAAGCGCTCGATG-----	430
Db	551	CTGAACAAGATCAAGAACGTGTGGCACACTCACTCAAGAAAGAGCTTGGACAGCAAC	610
Oy	431	---CGCCGGCTCAGGGCGGTCAATGTCGCGGCAAGCGCGCGGCAAGACACAAAGCCGA	487
Db	611	GGAGCTGCGCGCCCGCGCGGTGGCGGTGGCCGCCGCCGACATAGCCGCAAGCAGCCCA	670
Oy	488	AGAGCGCANAAGAACCCAGCCGCGCGCCGCGCGCGCGCGGTGCGCCGAGCGGTCG	547
Db	671	AGCGCGCAAAAGAGCGCCCGCGCGGTCAAGCGGAGGCGAGCGCGTCCGTCCGTACGCGTCGACA	730
Oy	548	CCTCGTCGTGGTGAACGAGTCTCTGATGGCTCGTCGTTGGCGGAGAGACAGGCAACG	607
Db	731	CCAGTAGCGGCGGTGACGTGCTCCACGATGACGAGTCGTGCGCGTGTGTCGCGCCGACGCG	790
Oy	608	CC 609	
Db	791	AC 792	

RESULT 2

US-10-449-902-11273
 ? Sequence 11273, Application US/10449902
 ? Publication NO. US20060123505A1
 ? GENERAL INFORMATION:
 ? APPLICANT: National Institute of Agrobiological Sciences.
 ? APPLICANT: Bio-oriented Technology Research Advancement Institution.
 ? APPLICANT: The Institute of Physical and Chemical Research.
 ? APPLICANT: Foundation for Advancement of International Science.
 ? TITLE OR INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
 ? FILE REFERENCE: MOA-A020511-US
 ? CURRENT APPLICATION NUMBER: US/10/449,902
 ? CURRENT FILING DATE: 2003-05-29
 ? PRIOR APPLICATION NUMBER: JP 2002-203269
 ? PRIOR FILING DATE: 2002-05-30
 ? PRIOR APPLICATION NUMBER: JP 2002-383870
 ? PRIOR FILING DATE: 2002-12-11
 ? NUMBER OF SEQ ID NOS: 56791
 ? SOFTWARE: PatentIn Ver. 2.1
 ? SEQ ID NO 11273
 ? LENGTH: 1399
 ? TYPE: DNA
 ? ORGANISM: Oryza sativa
 ? PUBLICATION INFORMATION:
 ? DATABASE ACCESSION NUMBER: AK108621
 ? DATABASE ENTRY DATE: 2002-08-28
 ? US-10-449-902-11273

Query Match	20.9%;	Score 251.8;	DB 6;	Length 1399;
Best Local Similarity	60.0%;	Pred. No. 5.5e-47;		
Matches 446;	Conservative 0;	Mismatches 282;	Indels 15;	Gaps 1

QY	62	GGGAAAGBACGACGACATAGGGGAGGGCTCCGTGTCGAGAGATAGGGGCTCAAGAGG	12
Db	104	GTGGGGGACCGCGCCATAGGGGAGGGCGCCGTGTTCGACAGAAAGGGGCTCAAGAGG	163
QY	122	GTTCATGAGCGCCGAGGAGAGACAAAGTCTCTCGTCGCCACATCCAGCGCCACGGCCACG	181
Db	164	GGCCCTGGAGCGCCGAGGAGAGACAACTCCTCGTCGACCTACATCCAGGCCAACGGCCACG	223
QY	182	GCAACTGGCGCGCCCTGCGCCCAAGCAAGCCGGGCTGCTGCGCTTGGCGCAAGGCTTGCCGCGC	241
Db	224	GCAAGCTGGCGCCTCTCCCAAGCTGCGAAGGGCTGAAACGGTGCGGCAAGAGCTGCGCGC	283
QY	242	TCCGTGGATCAACTACTGTGGCCCGGACATCAAGCGGGCAACTTCTCCAAAGAGAGG	301
Db	284	TGCGGTGGACGAATCACTCTCCGGCGGAGACTCAAGGCGCGGGCCCTTACCGCGGAGAGC	343

QY	302	AGGACACCATCATCCATCTCCACGAGCGCTGTGGAAACAGAGTGTCCCGCAATTGCGGCCCA	361
Db	344	AGAAATCATGTCTCAGCTCCACGGGCATCTGTGGCAACAAGTGTCTCATGATGCGGCGC	403
QY	362	GATTGCCCGGAGAGACGGACCAACGAGATCAAGAACGTGTGCAACACCTTCAGAAAGC	421
Db	404	AGTGCCTCGGCGCGGACCCGACCAACGAGATCAAGAACTATTGGAAACTCACTTCMAAAGC	463
QY	422	-----GCCCTCAATGGCGCGGCGCTCAAGGCGCGGTATGTCGAGCGGAGCGGCG	466
Db	464	AGCTGCGCGGAGTGGGCTTCGACGATTCGCGCCGCGCGGCGCGGCGGCGGCTGCCCGGCG	523
QY	467	GCAAGAAACACAAGAAAGCCGGAAGACGCGAAGAACGACGCGCGCGCGCGCGCGCGC	526
Db	524	CGCGTCATGAGCGGACGATGGGAGACCGCGCGGCTCGAAGGCGGAGGCGCGCTCTCCTCC	583
QY	527	CGGCGTCCGCGCGGAGGGGTCCGCTCTGTCTGTCTGTGACGGAAGTCTTCGATATGGCTCGTCCG	586
Db	584	TCTCTCTCTCCGCGCGTCCGCGGAGACGACGATCACCGCGCGCACACCACTCCCTCG	643
QY	587	TGGCGAAGAGACACGGCAACGCGCGGATACGCTCGGCGTCCGCGTCCGTGTGCGCAAGG	646
Db	644	CCTGTGCTCTCCACCAACCGCGGGGCGCGTGC CGCGCGCGCGAGCTACCGCGGAGACG	703
QY	647	AGGAGAGCTCTTCACTCTCGGCTTCCGAGGAATTCCAGATTCGACGACAGCTTCTGTGCG	706
Db	704	TGTTCTCTCGGCTCTCGAACTTCAGACATCGGGGAGCTCTTCGCAAGCTAGACCGTGTGG	763
QY	707	AGACGCTGTGATGCGCGTGGACGCGGTACGAGTGTCTCATGGAGCCCGCGACGCGTTCC	766
Db	764	CGCGCGGATCTGTCGTCTCCCTTCGCGGGGAGAGTCACTCAAGAGCGCTGTGAACAGAGAGG	823
QY	767	TCGCGCGCCATCCGCGCGACGAC	789
Db	824	AGGAGGCGCGCGCGCGCGGAC	846

RESULT 3

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US-10-449-902-10135
/ Sequence 10135, Application US/10449902
/ Publication No. US20060123505A1
/ GENERAL INFORMATION:
/ APPLICANT: National Institute of Agrobiological Sciences,
/ APPLICANT: Bio-oriented Technology Research Advancement Institution
/ APPLICANT: The Institute of Physical and Chemical Research.
/ APPLICANT: Foundation for Advancement of International Science.
/ TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USBS THEREOF
/ FILE REFERENCE: MOA-A0205Y1-US
/ CURRENT APPLICATION NUMBER: US/10/449,902
/ CURRENT FILING DATE: 2003-05-29
/ PRIOR APPLICATION NUMBER: JP 2002-203269
/ PRIOR FILING DATE: 2002-05-30
/ PRIOR APPLICATION NUMBER: JP 2002-383870
/ PRIOR FILING DATE: 2002-12-11
/ NUMBER OF SEQ ID NOS: 56791
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 10135
/ LENGTH: 1163
/ TYPE: DNA
/ ORGANISM: Oryza sativa
/ PUBLICATION INFORMATION:
/ DATABASE ACCESSION NUMBER: AK107483
/ DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-10135

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Query Match	20.6%	Score 248.2;	DB 6;	Length 1163;
Best Local Similarity	62.0%	Pred. No. 3.2e+46;		
Matches 416;	Conservative 0;	Mismatches 243;	Indels 12;	Gaps 1.

QY 75 ATGGGAGAGGAGCTCCGTGCTCGAGAAATGGGGCTCAAGAAAGGTCATGACGCCGGAG 138

Db 179 ATGGGAGAGGAGCGCGTGTCTCGACACAGAGTGGGGCTGAAAGAGGGGCCCTGACGCGCGAG 238

QY 139 GAGACAGAGTCTCTGCGCCATCAGCGCCAGCGCACTGGCGGCTT 198
DB 239 GAGACAGAGTCTCTGCGCCATCAGCGCCAGCGCACTGGCGGCTT 298
QY 199 CCCAGCAAGCCGCGCTGCTGCGGCAAGAGTCCGCTGCTGCTGCT 258
DB 299 CCCAGCAAGCCGCGCTGCTGCGGCAAGAGTCCGCTGCTGCTGCT 358
QY 259 CTGCGCGCGGCACTCAAGCGCGGCACTTCTCCAGAGAGAGAGACATCATTCAT 318
DB 359 CTGAGGCGCGCACTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 418
QY 319 CTGCAAG 378
DB 419 CTGCAAG 478
QY 379 GACCAAG 438
DB 479 GACCAAG 536
QY 439 CAGGCGGCTCATCTGCGCGGAGCGCGGAGAGAGAGAGAGAGAGAG 498
DB 537 -----GCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 596
QY 499 AAGCAG 558
DB 587 CCGGAG 646
QY 559 GTGACGAG 618
DB 647 GAG 706
QY 619 TCGGCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 678
DB 707 CCGGCG 766
QY 679 TTCAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 738
DB 767 TCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 826
QY 739 GTGTCATGGA 749
DB 827 GAGCCCATGTA 837

RESULT 4
US-10-449-902-5864
; Sequence 5864, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agricultural Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USBS THEROP
; FILE REFERENCE: MOA-A02051-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5864
; LENGTH: 1027
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK063027
; DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-5864

Query Match 18.9%; Score 227.6; DB 6; Length 1027;
Best Local Similarity 66.7%; Pred. No. 1.1e-41;
Matches 340; Conservative 0; Mismatches 169; Indels 1; Gaps 1;
QY 77 CAATGGGAGAGGCTCCGCTGCTGCGAGAGAGAGAGAGAGAGAGAGAG 136
DB 56 CGATGGGAGAGGCTCCGCTGCTGCGAGAGAGAGAGAGAGAGAGAGAG 115
QY 137 AG 196
DB 116 AG 175
QY 197 TGGCCAAAG 256
DB 176 TCCCAAG 235
QY 257 ACCTGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 316
DB 236 ACCTGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 295
QY 317 ATTCAG 376
DB 296 AGCTCAG 335
QY 377 CCGAG 435
DB 356 CCGAG 415
QY 436 GCTCAG 495
DB 416 GCTCAG 475
QY 496 AAG 555
DB 476 ACCTCAG 535
QY 556 TCGGAG 585
DB 536 GCGAG 565

RESULT 5
US-10-449-902-8691
; Sequence 8691, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agricultural Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USBS THEROP
; FILE REFERENCE: MOA-A02051-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 8691
; LENGTH: 1139
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK106039
; DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-8691

Query Match 18.6%; Score 223.6; DB 6; Length 1139;
Best Local Similarity 68.8%; Pred. No. 8.7e-41;
Matches 307; Conservative 0; Mismatches 139; Indels 0; Gaps 0;

QY 79 ATGGGAGGAGCTCCCTGCTCGAGAGATGGGGCTCAAGAGGCTCATGAGCGCGGAG 138
DB 187 ATGGGAGGAGAGCCCTGCTCGAGAGAGCTGGGGGTGAAGAGGGGCGCTGAGCGCGGAG 246
QY 139 GAGGACAAAGTCTCTGTCGCGCCCAATCCAGCGCCCAAGGAGAACTGGCGCGCTG 198
DB 247 GAGGACAAAGAGCTATGAGCTTCACTCGAGCAACCGGCAATTTGCTGCGCGCGCTG 306
QY 199 CCGAAGCAAGCGCGGCTGCTGCTGGTGGCGCAAGAGCTGCGGCTCCGCTGATCAACTAC 258
DB 307 CCGAAGCTGCGCGGCTGCTGCTGGCGCAAGAGCTGCGCTCCGCTGGGCAAACTAC 366
QY 259 CTGGCGCGGAGATCAAGCGGGGCAACTCTCCAAAGAGAGAGAGCAACATCATCCAT 318
DB 367 CTGGCGCGGAGATCAAGCGGGGCAACTCTCCAAAGAGAGAGAGCAACATCATCCAT 426
QY 319 CTCCAGAGCTCTTGGCAACAGTGTGTCGCAATTTGCCCGCAGGTTGGCCGGAGAGAG 378
DB 427 CTCCAGCGCAAGCTCGGCAACAGTGTGTCGCAATTTGCCCGCAGGTTGGCCGGAGAG 486
QY 379 GACAACGAGATCAAGAGCTGTGGCAACCCACCTCAAGAGCGCTCGATGCGCGCT 438
DB 487 GACAACGAGATCAAGAGCTGTGGCAACCCACCTCAAGAGCGCTCGATGCGCGCT 546
QY 439 CAGGCGGCTCATGTGCGCGCGAGCGCGCGCAAGAGCAAGAGCGCGAGAGCGGAG 498
DB 547 ATCGACCGCGGTGACGAGCGCGCTCTCGACCGAGAGAGAGAGCGCGCGAGAGCG 606
QY 499 AAGCGAGCG 524
DB 607 CAGTCCACCGGTGACGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 632

RESULT 6
US-10-953-349-33713
; Sequence 33713, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 33713
; LENGTH: 1284
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (736)..(736)
; OTHER INFORMATION: n is a, c, g, or t
US-10-953-349-33713

Query Match 18.5%; Score 222.8; DB 6; Length 1284;
Best Local Similarity 78.8%; Pred. No. 1,4e-40;
Matches 279; Conservative 0; Mismatches 72; Indels 3; Gaps 1;
QY 77 CATGGGAGAGGCTCCGTGCTCGAGAGATG---GGGCTCAAGAGAGGTCATGAGCGC 133
DB 125 CGATGGGAGGCTCGCTGCTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 184
QY 134 CGAG 193
DB 185 CCGAG 244
QY 194 CCTGCGCGAG 253
DB 245 CGCTGCGCGAG 304
QY 254 ACTACTGCGCGAG 313

DB 305 ACTACTGCGCGAG 364
QY 314 TCCATCTCCAG 373
DB 365 TCCAGCTCCAG 424
QY 374 GAG 427
DB 425 GAG 478

RESULT 7
US-10-449-902-7552
; Sequence 7552, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agricultural Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A02051-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7552
; LENGTH: 1389
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK064679
; DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-7552

Query Match 18.1%; Score 217.8; DB 6; Length 1389;
Best Local Similarity 76.5%; Pred. No. 1.8e-39;
Matches 267; Conservative 0; Mismatches 82; Indels 0; Gaps 0;
QY 78 AATGGGAGAGGCTCCGTGCTCGAGAGATGGGGCTCAAGAGGTCATGAGCGCGGAG 137
DB 149 AATGGGAGAGGAGCGCTGCTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 208
QY 138 GAG 197
DB 209 GAG 268
QY 198 GCGCAAG 257
DB 269 CCGCAAG 328
QY 258 CCGGAG 317
DB 329 CCGGAG 388
QY 318 TCTTCAG 377
DB 389 CCGGAG 448
QY 378 GAG 426
DB 449 GAG 497
RESULT 8
US-10-449-902-2899
; Sequence 2899, Application US/10449902
; Publication No. US20060123505A1

```
GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USBS THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2899
LENGTH: 1037
TYPE: DNA
ORGANISM: Oryza sativa
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK060684
DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-2899
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Query Match      18.1%; Score 217.6; DB 6; Length 1037;
Best Local Similarity 59.5%; Pred. No. 1.8e-39;
Matches 389; Conservative 0; Mismatches 259; Indels 6; Gaps 1;
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OY 79 ATGGGAGGAGGCTCCGTCGCGAGAGATGGGCTCAGAGAGGATCATAGACGCCGAG 138
DB 97 ATGGGAGGATCGCATGCTGCGAGAGGCGCACAGACAGAGGGGCGTGGAGAGAGG 156
OY 139 GAGGACAGAGTCTCTCGCCCATTCACAGCCGACCGCCAGCGCACTGGCGCCCTG 198
DB 157 GAGGACCAAGCGGTGATCGCTCATCAAGCCGACGCGAGGGTGTGGCGGTGCTG 216
OY 199 CCCAAGCAAGCGGGGCTGCTGCGCGCAAGAGTGGCGGCTCGGTGGATCACTCA 258
DB 217 CCCAAGCGGGGCGGCTCTCTCGCGCGAGAGAGTGGCGGCTCGGTGGATCACTCA 276
OY 259 CTGCGGCGCGAGATCAAGCGGGGCACTTCTCCAGAGAGAGAGACACATCATCAT 318
DB 277 CTCGCGCCCGACTCAAGCGCGGCACTTCAAGAGAGAGAGAGAGAGAGAGAGAG 336
OY 319 CTCACAGAGCTGTTGGGCAACAGTGTGCTCGCAATTCGCGGCACTTGGCGGAGAG 378
DB 337 CTCACAGCTTCTCGGCAACAGTGTGCTGATTGCGGGGCACTTGGCGGAGAGAG 396
OY 379 GACACGAGATCAAGAACTGAGGACAGGACATCAAGCGGCAAGCTCTGAGAGAG 438
DB 397 GACACGAGATCAAGAACTGAGGACAGGACATCAAGCGGCAAGCTCTGAGAGAG 456
OY 439 CAGGGCGGTATGT-----CGGCGAGCGGCGGCGGCAAGAGACAAAGCGAGAGC 492
DB 457 ATGACACCGGACAGGACCGGCGGCTCAGCGCCGGAAGAGAGCGCCCGCGGAGCG 516
OY 493 GCGAAGAACCAAGCGCGCGCGCGCGCGCGCGCGCGCTGCGCGAGCGGTGCGCTTG 552
DB 517 CTGACCAAGCGGCGGACAGCGCGCGCTTTCCTTCCCTTGGCGCGCGCGCGCGAG 576
OY 553 TGTGTGATGACGAGAGCTCTGATGAGGCTGTGCTGGTGGCGGAGAGAGAGAGAG 612
DB 577 CAGCAGAGCTTACACAAACCGGAGAGAGCGCGCGCGCGCGAGATCGAGCTTTCGAG 636
OY 613 ATCAGCTCGGCGCTCGCGCTCGGTGCGCGGCAAGAGAGAGAGCTTTCAGCTTCG 672
DB 637 TCGCGGCGGTCCCGCGCGTGGAGAGAGCGGACAGAGAGAGCGCGGAGCTGAGAG 696
OY 673 GAGGAGTTTCAAGATGACAGAGAGCTTCTGCTCGGAGAGAGCTTTCAGCTTCG 726
DB 697 CCGCGGTGCGCGGAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCA 750
```

```
RESULT 9
US-10-449-902-26232
Sequence 26232; Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USBS THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 26232
LENGTH: 995
TYPE: DNA
ORGANISM: Oryza sativa
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK101674
DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-26232
```

```
Query Match      18.1%; Score 217.4; DB 6; Length 995;
Best Local Similarity 76.7%; Pred. No. 1.9e-39;
Matches 266; Conservative 0; Mismatches 81; Indels 0; Gaps 0;
```

```
OY 71 CAAGCAATATGGGAGAGGCTCCGTCGCGAGAGATGGGCTCAGAGAGGCTCATGGA 130
DB 109 CATGCACTATGAGAGCGCGCTGTCGACAGAGACCGGCTCAAGAGAGGCGCTGGA 168
OY 131 CGCGGAGAGAGGCAAGAGTCTGTCGCGCAATCCAGCGGCGGCAAGAGAGAGAG 190
DB 169 CGCGGAGAGAGAGGCTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 228
OY 191 GCGGCTGCGGCAAGAGCGGCGGCTGCTGTCGCGCAAGAGAGAGAGAGAGAGAG 250
DB 229 GCGGCTGCGGCAAGAGCGGCGGCTGCTGTCGCGCAAGAGAGAGAGAGAGAGAG 288
OY 251 TCAACTACTGCGGCGGCGGCAATCAAGCGGCGGCACTTCTCAAGAGAGAGAGAG 310
DB 289 CCAACTACTGAGGCGCGGAGATCAAGCGGAGAACTTCAAGCGGAGAGAGAGAG 348
OY 311 TCATCATCTGCAAGAGAGTGTGCAAGAGAGTGTGCGCAATTCGCGGAGAGAGAG 370
DB 349 TGTCACTCTCAAGAGAGTGTGCTGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAG 408
OY 371 GAGGAGAGAGAGAGAGATCAAGAGAGTGTGCGAGAGAGAGAGAGAGAGAGAGAG 417
DB 409 AGGAGAGAGAGAGAGAGATCAAGAGAGTGTGCGAGAGAGAGAGAGAGAGAGAGAG 455
```

```
RESULT 10
US-10-449-902-3902
Sequence 3902; Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USBS THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
```

;; PRIOR FILING DATE: 2002-12-11
;; NUMBER OF SEQ ID NOS: 56791
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 3902
;; LENGTH: 1087
;; TYPE: DNA
;; ORGANISM: Oryza sativa
;; PUBLICATION INFORMATION:
;; DATABASE ACCESSION NUMBER: AK061437
;; DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-3902

Query Match 18.1%; Score 217; DB 6; Length 1087;
Best Local Similarity 75.1%; Pred. No. 2,4e-39;
Matches 271; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

QY 77 CAATGGGAGGAGCTCCGTCTGCGAGAGATGGGCTCAAGAGGATCCATGAGCGCCG 136
DB 107 CCATGGGAGGAGCTCCGTCTGCGAGAGATGGGCTCAAGAGGATCCATGAGCGCCG 166
QY 137 AGGAGGACAGGTCTCTGCGCCCAATCCAGCGCCCAAGCGCACTGGCGGCC 196
DB 167 AGGAGGACATCTCTCTGCTCTCTACATCAAGAACCGCCCGCACTGGAATCG 226
QY 197 TGGCCCAAGAGCGCGGCTGCTGCGTGGCGGCAAGAGCTGCCGCTCCGATCACT 256
DB 227 TTCCCATCAACTGCGGCTGATGAGTGACGACAGAGCTGCGGCTGGAGCACT 286
QY 257 ACCTGGGCGGACATCAAGCGGCGCACTTCTCAAGAGAGAGACACCATCATCC 316
DB 287 ACCTGGGCGGAGATCAAGCGGCGCACTTCAAGAGAGAGAGAGATCATGCTC 346
QY 317 ATCTCCAGAGCTGCTGGCAACAGTGTGCTCAATTCGCCGAGTTCGCCGAGAG 376
DB 347 ACCTCCAGTGTCTTCTGGCAACCGCTGGCGGCACTTCTCACTCCCGCAGCG 406
QY 377 CGGACACGAGATCAAGAGAGTGTGGCAACCCACTCAAGAGCGCTCGATGCGCGG 436
DB 407 CGGACACGATCAAGAGAGTGTGGCAACCCACTCAAGAGAGCTCGCGCGCG 466

QY 437 C 437
DB 467 C 467

RESULT 11
US-10-449-902-11361
Sequence 11361, Application US/10449902
Publication No. US20060123505A1

;; GENERAL INFORMATION:
;; APPLICANT: National Institute of Agricultural Sciences.
;; APPLICANT: Bio-oriented Technology Research Advancement Institution.
;; APPLICANT: The Institute of Physical and Chemical Research.
;; APPLICANT: Foundation for Advancement of International Science.
;; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
;; FILE REFERENCE: MOA-A02051-US
;; CURRENT APPLICATION NUMBER: US/10/449,902
;; CURRENT FILING DATE: 2003-05-29
;; PRIOR APPLICATION NUMBER: JP 2002-203269
;; PRIOR FILING DATE: 2002-05-30
;; PRIOR APPLICATION NUMBER: JP 2002-383870
;; PRIOR FILING DATE: 2002-12-11
;; NUMBER OF SEQ ID NOS: 56791
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 11361
;; LENGTH: 1031
;; TYPE: DNA
;; ORGANISM: Oryza sativa
;; PUBLICATION INFORMATION:
;; DATABASE ACCESSION NUMBER: AK108709
;; DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-11361

Query Match 17.7%; Score 212.4; DB 6; Length 1031;
Best Local Similarity 75.4%; Pred. No. 2,5e-38;
Matches 264; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

QY 79 ATGGGAGGAGCTCCGTCTGCGAGAGATGGGCTCAAGAGGATCCATGAGCGCCGAG 138
DB 87 ATGGGAGGAGCTCCGTCTGCGAGAGATGGGCTCAAGAGGAGGAGGAGGAGCGCCGAG 146
QY 139 GAGGACAGGCTCTGCGCCCAATCCAGCGCCCAAGCGCACTGGCGGCCCGG 198
DB 147 GAGGACAGGAGCTCTCTCTCTCTCAATGCGCATGCTGCTGGAGGCTGCTG 206
QY 199 CCCAAGCAGAGCGGCTCTGCGTGGCGCAAGAGCTCCGCTCCGATCACTAC 258
DB 207 CCCAAGCTCCAGGCTCTGCGTGGCGCAAGAGCTCCGCTCCGATGAGGAGGAGGAG 266
QY 259 CTGGGCGGAGATCAAGCGGCGCACTTCTCAAGAGAGAGAGAGACCATCATCT 318
DB 267 CTGGGCGGAGATCAAGCGGCGCACTTCTCTCTCAATGCGCATGCTGCTGGAGGCTG 326
QY 319 CTCCAGAGGCTCTGCGCAAGAGTGTCCGCAATTCGCCGAGGTTGCCGAGGAGAG 378
DB 327 CTCCAGAGGAGCTCTGCGCAAGAGTGTCCGCAATTCGCCGAGGTTGCCGAGGAGAG 386
QY 379 GACACGAGATCAAGAGAGTGTGGCAACCCACTCAAGAGAGGCGCTCGA 428
DB 387 GACACGAGATCAAGAGAGTGTGGCAACCCACTCAAGAGAGGAGGAGGAGGAGGAG 436

RESULT 12
US-10-449-902-1122
Sequence 1122, Application US/10449902
Publication No. US20060123505A1

;; GENERAL INFORMATION:
;; APPLICANT: National Institute of Agricultural Sciences.
;; APPLICANT: Bio-oriented Technology Research Advancement Institution.
;; APPLICANT: The Institute of Physical and Chemical Research.
;; APPLICANT: Foundation for Advancement of International Science.
;; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
;; FILE REFERENCE: MOA-A02051-US
;; CURRENT APPLICATION NUMBER: US/10/449,902
;; CURRENT FILING DATE: 2003-05-29
;; PRIOR APPLICATION NUMBER: JP 2002-203269
;; PRIOR FILING DATE: 2002-05-30
;; PRIOR APPLICATION NUMBER: JP 2002-383870
;; PRIOR FILING DATE: 2002-12-11
;; NUMBER OF SEQ ID NOS: 56791
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 1122
;; LENGTH: 1042
;; TYPE: DNA
;; ORGANISM: Oryza sativa
;; PUBLICATION INFORMATION:
;; DATABASE ACCESSION NUMBER: AK104053
;; DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-1122

Query Match 17.5%; Score 209.8; DB 6; Length 1042;
Best Local Similarity 62.8%; Pred. No. 9,4e-38;
Matches 350; Conservative 0; Mismatches 192; Indels 15; Gaps 1;

QY 77 CAATGGGAGGAGCTCCGTCTGCGAGAGATGGGCTCAAGAGGATCCATGAGCGCCG 136
DB 132 CCATGGGAGGAGCTCCGTCTGCGAGAGATGGGCTCAAGAGGAGGAGGAGGAGGAGGAG 191
QY 137 AGGAGGACAGGTCTCTGCGCCCAATCCAGCGCCCAAGCGCACTGGCGGCC 196
DB 192 AGGAGGACAGGCTCTCTGCGCCCAATCCAGCGCCCAAGCGCACTGGCGGCC 251
QY 197 TGGCCCAAGAGCGGCGGCTGCTGCGTGGCGGCAAGAGCTCCGATCACT 256
DB 252 TGGCCCAAGAGCGGCGGCTCTCTCTCTCTCAATGCGCATGCTGCTGGAGGAGGAGGAG 311

WT CUEM EEC CEV ADI DOT

267 241

```
RESULT 2
US-10-425-115-222820
; Sequence 222820, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425.115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 222820
; LENGTH: 295
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_134802C.1.pep
US-10-425-115-222820

Query Match          67.3%; Score 920; DB 4; Length 295;
Best Local Similarity 67.3%; Pred. No. 5.2e-73;
Matches 202; Conservative 9; Mismatches 41; Indels 48; Gaps 12;

QY 1 MGRAPCEKMGKKGKGPWTPEEDKVLVAHIQRHGHGNWRALPKQAGLLRCGKSCRLRWINY 60
DB 1 MGRAPCEKMGKKGKGPWTPEEDKVLVAHIQSFHGNWRALPKQAGLLRCGKSCRLRWINY 60
QY 61 LRPDIKRGNFSKEEBDTIITLHELIGNRWSAIAARLPGRTDNEIKVWHTLKKRLDAPA 120
DB 61 LRPDIKRGNFSKEEBDAIITLHELIGNRWSAIAARLPGRTDNEIKVWHTLKKRLDPTK 120
QY 121 Q-----GGHVAASGGKKKKPKSAK-----PA-AAAAAPASPERS 156
DB 121 QEQQOQHGTTPAAGAGKGRPAALAAKRGCGGAKATADAVVPAAPATAPASPERS 180
QY 157 -ASSSVTESSMASSVAEHEGNAGISSASASVCAKESSSPTSAS--BEFOIDSPWSETLS 213
DB 181 AASSSVTESSMTQ--EQEHGNTGSSPA---FPKESELTTSSSDAEBFQDFDSFWESETLS 235
QY 214 MPDGDID--VSMPPG-DAF-----VAPPSAD-----DMDYVLGVFMESGEA-Q-DLPQI 257
DB 236 MPDLSLDVVPMEPSDDAFGDVDVDVAAASSSSVGAADGDLDYWLRFVMEGDAHPQLPQI 295

RESULT 3
US-10-425-115-343620
; Sequence 343620, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425.115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 343620
; LENGTH: 279
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(279)
; OTHER INFORMATION: unsure at all Xaa locations
```

```
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_76543C.1.pep
US-10-425-115-343620

Query Match          65.2%; Score 892; DB 4; Length 279;
Best Local Similarity 64.6%; Pred. No. 1.5e-70;
Matches 186; Conservative 18; Mismatches 44; Indels 40; Gaps 11;

QY 1 MGRAPCEKMGKKGKGPWTPEEDKVLVAHIQRHGHGNWRALPKQAGLLRCGKSCRLRWINY 60
DB 1 MGRAPCEKMGKKGKGPWTPEEDKVLVAHIQSFHGNWRALPKQAGLLRCGKSCRLRWINY 60
QY 61 LRPDIKRGNFSKEEBDTIITLHELIGNRWSAIAARLPGRTDNEIKVWHTLKKRLDAPA 120
DB 61 LRPDIKRGNFSKEEBDAIITLHELIGNRWSAIAARLPGRTDNEIKVWHTLKKRLDPTK 120
QY 121 Q-----GGHVAASGGKKKKPKSAK-----KPAAAAAP-----PASPERS-ASSSVTESS 165
DB 121 KQLEQOHGAHAGDPAARSRPRKAGARXKTTAAVAPATTAAPASPERSAASSSVTEST 180
QY 166 MASSVAEHEGNAGISSASASVCAKESSSPTSAS--ASEFOIDSPWSETLSMPIDGY-DV 221
DB 181 -----EQEGNTGTSSPG---FPKESELTSSSEAAEBFQDFDTSFWSSETLSMPIDSDV 231
QY 222 SMEP-----GDAFVAPPSAD-----DMDYVLGVFMESGEA-QDLPQI 257
DB 232 PTEPCSSGAFGDPVAASSSSSVGADADLDYWLGVFMKSGDAHQQLPQV 279
```

```
RESULT 4
US-11-087-099-10942
; Sequence 10942, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Apad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087, 099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 10942
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Hordeum vulgare
US-11-087-099-10942

Query Match          61.1%; Score 835.5; DB 6; Length 288;
Best Local Similarity 64.7%; Pred. No. 1.6e-65;
Matches 180; Conservative 12; Mismatches 47; Indels 39; Gaps 7;
```

```
QY 16 PWTPEEDKVLVAHIQRHGHGNWRALPKQAGLLRCGKSCRLRWINYLRPDIKGNFSKEE 75
DB 14 PVDAAECKTLVAHIHSHGHGNWRALPKQAGLLRCGKSCRLRWINYLRPDIKGNFSDEE 73
QY 76 DTIITLHELIGNRWSAIAARLPGRTDNEIKVWHTLKKRLDAPAQGGHVAASGGKQHK 135
DB 74 QSIQLHQLGNRWSAIAARLPGRTDNEIKVWHTLKKRLDPSAQEQEBAKAKK 133
QY 136 PKSAK-----KPAAAAAAPASPERSASSSVTES--SMASVVAEHN 176
DB 134 PAAAAAPRRKDGKVMRLNALTRAAAAAASVSSESVSTVESTSTAABAOHGN 193
QY 177 AGISSASASVCAKESSSPTSAS--SEFOIDSPWSETLSMPIDGY-DVSMPPGDAFVAP 233
DB 194 SGSSSASASASYKE-CFTSSESEBFQIDBSFWSSETLSMPIDLDLNDVCMERHDAKCPD 252
QY 234 SADMDYVLGVFMESG-----EAQDLPQI 257
DB 253 G--DMDYWLRLFMEGGGSGSGSDNNNNHDGALDLPQI 288
```

```
RESULT 5
US-09-443-704-4
```

Query Match	60.5%	Score 827.5	DB 4	Length 258
Best Local Similarity	62.1%	Pred. No. 6.9e-65		
Matches 169, Conservative	29	Mismatches 45	Indels 29	Gaps 8

227 C A E B C E N D D M D N E W I Y I E T O A C C M O N T D O T 250

Db 227 GASFSSNDMDDFWLKLFIQAGGMQLPQI 258

```

RESULT 9
US-11-096-568A-25632
: Sequence 25632, Application US/11096568A
: Publication NO. US20060048240A1
: GENERAL INFORMATION:
: APPLICANT: Alexandrov, Nikolai et al.
: TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
: TITLE OF INVENTION: Theory
: FILE REFERENCE: 2750-1592PUS2
: CURRENT APPLICATION NUMBER: US/11/096, 568A
: CURRENT FILING DATE: 2005-04-01
: NUMBER OF SEQ ID NOS: 34471
: SEQ ID NO 25632
: LENGTH: 309
: TYPE: PRT
: ORGANISM: Zea mays subsp. mays
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)..(309)
: OTHER INFORMATION: Ceres Seq. ID no. 15222886
US-11-096-568A-25632

```

Query Match	58.4%;	Score 799.5;	DB 6;	Length 309;
Best Local Similarity	58.8%;	Pred. No. 2.7e-62;		
Matches 160;	Conservative 30;	Mismatches 51;	Indels 31;	Gaps 8;

```

RESULT 10
US-10-425-115-335937
Sequence 335937, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425.115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 335937
LENGTH: 261
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(261)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: MWT4577_69483C.1.pep
US-10-425-115-335937

```

	Query Match	58.0%	Score 793.5:	DB 4:	Length 261:
	Best Local Similarity	57.5%:	Pred. No. 7.3e-62:		
	Matches 157:	Conservative 31:	Mismatches 56:	Indels 29:	Gaps 7
OY	1	MGRAPCCCKWGLKKGPWTPEEDKVLVAHIQRHGHGNMRALPK-QAGLLRCGSKSCLRLWIN	59		
Db	1	MGRSPCCCKMGLKKGPMTAEEDRILVAVERIGHGNMPALPKQOAGLLRCGSKSCRIRWIN	60		
OY	60	YLRPDIKRGNSKEEEDTIIHLHELLGNRWSAIAARLPRTONEIKNVHTLKKRLDAP	119		
Db	61	YLRPDIKRGNSREEDDAIQLHQMLGNRWSTIAARLPGRITNELKNVHTHLKKRLDEK	120		
OY	120	AOGGHVAASGKRKHKKPKRSACKPPA-----AAAPASPBPERSAS--SYTBESMASSVAB	172		
Db	121	PASQOAPRRKRTTKQQOPREPEPVTLLEGPAVAPVPBPSRLSTTTSTTTADVSAAIS	180		
OY	173	EHGNAIGISSASVCAKEESSFTSASEFOJDDSFMSSETLSM--PLUDGYDVSMEP-----	225		
Db	181	SLENNG-----DSFTSBEDYYQIDDSFMSSETLTANTTYIVDSFGVQQAKSGSF	227		
OY	226	GDATFAVAPPSSA-DDMDYMLGVFMESGEADDLPPI	257		
Db	228	GKSAAPBSTDDMDFWLKLFEMQASDMQNLPPI	260		


```

; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 42619
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAV03-C81473_1.pep
US-10-767-701-42619
```

```

Query Match          51.7%; Score 707; DB 4; Length 200;
Best Local Similarity 72.0%; Pred. No. 2,4e-54;
Matches 139; Conservative 7; Mismatches 35; Indels 12; Gaps 3;
```

```

QY      1 MGRAPCCCKMGLKKGPTPEEDKVLVAHIQRHGHGNMRALPKOAGLLRCGKSCRLRWINY 60
        |||
DB      1 MGRAPCCCKMGLKKGPTPEEDKVLVAHIQSFHSHMRALPKOAGLLRCGKSCRLRWINY 60
        |||
QY      61 LRPDIKRGNFSKEEDTIIHLHELGNRWSAIAARLPGRTDNEIKVWHTHLKKRLDAPA 120
        |||
DB      61 LRPDIKRGNFSKEEDAIITLHEQLGNRWSAIAARLPGRTDNEIKVWHTHLKKRLPTT 120
        |||
QY      121 ----QGGHVAASGGKHKKKPKSAKKPAAA-----AAAPPAPEPS-ASSSTESSMAS 168
        |||
DB      121 KPBEQGAQAGAGAGKGRPRGAAKTTADVAVPATTAVPSPSPASSSVTESSSMT 180
        |||
QY      169 SVAEHEGNAGISS 181
        :|
DB      181 EOEQEGNTGSSA 193
        :|
```

```

RESULT 15
US-10-437-963-110428
; Sequence 110428, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 110428
; LENGTH: 276
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_14495C.1.pep
US-10-437-963-110428
```

```

Query Match          51.0%; Score 697.5; DB 4; Length 276;
Best Local Similarity 53.2%; Pred. No. 2.5e-53;
Matches 150; Conservative 34; Mismatches 61; Indels 37; Gaps 10;
```

```

QY      118 --APAQGGHVAASGGKK---HKPKSAKKPAAA--AAAPPAPEPSAS---SSVTESSMA 167
        |||
DB      121 KLAAGGG-----GGRPHTRKQPYAAKSAAVKKEATPSVDTSSGVTCTVTESS-P 174
        |||
QY      168 SVAEHEGNAGISASASVCAKESSPTSASE-----EFOIDSFWSET---LS 213
        |||
DB      175 SSADGDHRRQOQOTQHAAV---KEESFSGGELPAAAAAFTAAADWDESFWSSTEVTKMM 231
        |||
QY      214 MPLDGYDVSME--PGDAFVAFPSPADMDYVLGVFMESGEAODL 254
        |||
DB      232 AGLDGMDDELAIAGTSSAAAPASDDMEFWLKMLLSGDWRL 273
        |||
```

```

Search completed: June 24, 2006, 00:08:43
Job time : 187 secs
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 24, 2006, 00:05:47 ; Search time 22 Seconds

(without alignments)
266.878 Million cell updates/sec

Title: US-10-521-811-2

Perfect score: 1368

Sequence: 1 MGRAPCCCKMKGLKGPWTPB.....MDYVLGVFMESGEADLPQI 257

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 99297 seqs, 22845552 residues

Total number of hits satisfying chosen parameters: 99297

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:*

- 1: /EMC_Celerra_SIDS3/prodata/1/pubppaa/US09_NEW_PUB.pep:*
- 2: /EMC_Celerra_SIDS3/prodata/1/pubppaa/US06_NEW_PUB.pep:*
- 3: /EMC_Celerra_SIDS3/prodata/1/pubppaa/US07_NEW_PUB.pep:*
- 4: /EMC_Celerra_SIDS3/prodata/1/pubppaa/US08_NEW_PUB.pep:*
- 5: /EMC_Celerra_SIDS3/prodata/1/pubppaa/PCT_NEW_PUB.pep:*
- 6: /EMC_Celerra_SIDS3/prodata/1/pubppaa/US10_NEW_PUB.pep:*
- 7: /EMC_Celerra_SIDS3/prodata/1/pubppaa/US11_NEW_PUB.pep:*
- 8: /EMC_Celerra_SIDS3/prodata/1/pubppaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	697.5	51.0	276	6	US-10-449-902-40114 Sequence 40114, A
2	661.5	48.4	285	6	US-10-953-349-9699 Sequence 9699, AP
3	658	48.1	275	6	US-10-953-349-22502 Sequence 22502, A
4	658	48.1	320	6	US-10-953-349-22501 Sequence 22501, A
5	612	44.7	266	6	US-10-953-349-22503 Sequence 22503, A
6	606.5	44.3	276	6	US-10-953-349-9700 Sequence 9700, AP
7	544	39.8	267	6	US-10-449-902-38592 Sequence 38592, A
8	544	39.8	300	6	US-10-449-902-39724 Sequence 39724, A
9	524	38.3	266	6	US-10-449-902-34326 Sequence 34326, A
10	523	38.2	331	6	US-10-953-349-33714 Sequence 33714, A
11	511	37.4	260	6	US-10-449-902-29589 Sequence 29589, A
12	511	37.4	260	6	US-10-449-902-44757 Sequence 44757, A
13	511	37.4	260	6	US-10-449-902-47791 Sequence 47791, A
14	507.5	37.1	311	6	US-10-449-902-32367 Sequence 32367, A
15	502.5	36.7	342	6	US-10-953-349-10216 Sequence 10216, A
16	502.5	36.7	311	6	US-10-953-349-10215 Sequence 10215, A
17	500	36.5	274	6	US-10-953-349-16711 Sequence 16711, A
18	498	36.4	255	6	US-10-449-902-39812 Sequence 39812, A
19	495.5	36.2	282	6	US-10-953-349-8309 Sequence 8309, AP
20	485	35.5	330	6	US-10-449-902-41941 Sequence 41941, A
21	484.5	35.4	279	6	US-10-449-902-36011 Sequence 36011, A
22	484	35.4	251	6	US-10-449-902-31755 Sequence 31755, A
23	484	35.4	251	6	US-10-449-902-32100 Sequence 32100, A
24	484	35.4	427	6	US-10-449-902-31540 Sequence 31540, A
25	479.5	35.1	236	6	US-10-953-349-5012 Sequence 5012, AP

26	476	34.8	285	6	US-10-449-902-37148 Sequence 37148, A
27	475	34.7	152	6	US-10-449-902-54567 Sequence 54567, A
28	475	33.9	275	6	US-10-449-902-39353 Sequence 39353, A
29	464	33.9	289	6	US-10-449-902-39555 Sequence 39555, A
30	453	33.1	265	6	US-10-953-349-16712 Sequence 16712, A
31	450	33.1	315	6	US-10-953-349-24254 Sequence 24254, A
32	435	31.8	261	6	US-10-953-349-18959 Sequence 18959, A
33	421.5	30.8	264	6	US-10-449-902-40228 Sequence 40228, A
34	415	30.3	281	6	US-10-449-902-40718 Sequence 40718, A
35	409.5	29.9	308	6	US-10-953-349-22671 Sequence 22671, A
36	409.5	29.9	337	6	US-10-953-349-22670 Sequence 22670, A
37	408	29.8	273	6	US-10-449-902-38244 Sequence 38244, A
38	403.5	29.5	270	6	US-10-953-349-25120 Sequence 25120, A
39	403.5	29.5	302	6	US-10-953-349-25119 Sequence 25119, A
40	402	29.4	258	7	US-11-179-064B-76 Sequence 76, Appl
41	394.5	28.8	285	6	US-10-449-902-47099 Sequence 47099, A
42	394.5	28.8	289	6	US-10-449-902-50726 Sequence 50726, A
43	382	27.9	341	6	US-10-953-349-22876 Sequence 22876, A
44	380	27.8	300	6	US-10-449-902-56335 Sequence 56335, A
45	380	27.8	474	6	US-10-449-902-35273 Sequence 35273, A

ALIGNMENTS

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RESULT 1
US-10-449-902-40114
; Sequence 40114, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 40114
; LENGTH: 276
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-40114

Query Match      51.0%; Score 697.5; DB 6; Length 276;
Best Local Similarity 53.2%; Pred. No. 8.3e-44;
Matches 150; Conservative 34; Mismatches 61; Indels 37; Gaps 10;

OY      1 MGRAPCCCKMKGLKGPWTPBEEKVLVAHIORHCHGNWRALPKOAGLRCGSKRLRWINY 60
      |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB      1 MGRAPCCCKMKGLKGPWTPBEEKVLVAHIORHCHGNWRALPKOAGLRCGSKRLRWINY 60
      |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

OY      61 LRDDIKRGNFSKEEDTIIHLHLLGNRWSAIALPGRDNEIKVWHTLKKRLD-- 117
      |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB      61 LRDDIKRGNFTADEEDLIVLHNSLGNRWSAIAQVGRDNEIKVWHTLKKRLD-- 120
      |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

OY      118 --APAGGHHVAGSGGK--HKPKKAKKPA--AAAPASPERAS--SSVTSSMA 167
      |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB      121 KLAAGGCG--GGRPHTRKQPKAKAAVREATPSVSDTSSGVTCSTVTESS-P 174
      |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

OY      168 SVAEEHGNAGTSSASASVCAKEESFTSASE-----EFOIDDSFWSFT---LS 213
      |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB      175 SSADGHRKQOQOQTOHAIV---KEESFSSGGELPAPAAAPTAAMDDESFWSSTVTCGM 231
      |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

OY      214 MPLDGYDVSM-PGDAFVAPPSADMDVWLVGVFMESGEADLP 254
      |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB      232 AGIGDMDEELIAGTSSAAARSDDMEFWLKMLESQDMRDL 273
      |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
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RESULT 2
US-10-953-349-9699
; Sequence 9699, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9699
; LENGTH: 285
; TYPE: PRP
; ORGANISM: Arabidopsis thaliana
US-10-953-349-9699

Query Match 48.4%; Score 661.5; DB 6; Length 285;
Best Local Similarity 49.0%; Pred. No. 3.5e-41;
Matches 146; Conservative 25; Mismatches 66; Indels 61; Gaps 6;
QY 1 MGRAPCCCKMGLKGPWTPBEDKVLVAHIQRHGNMRAIPKQAGLLRCCKSCRLRWINY 60
DB 1 MGRAPCCCKMGLKGPWTPBEDQILVSFIINHSHMRAIPKQAGLLRCCKSCRLRWINY 60
QY 61 LRPDIRKGNFSEEDTIIHLHLLGNRWSAIAARLPGRTDNEIKVMWHTLKKRLDAPA 120
DB 61 LRPDIRKGNFTKEEDAIISLHQLGNRWSAIAAKLPGRDNEIKVMWHTLKKRLD- 119
QY 121 QGGHVAASGGKHKHKKPKSAKPPAAAAAPPASPERSSSVTSSMASSVAEEHGNAGIS 180
DB 120 QPAKPTSNKKGKTKPKS-----ESVITSSNSTRESEELADS-----SNPSGES 163
QY 181 SASASYCAKESSFTSA-----FOIDSPMSET 211
DB 164 LFTSPSTSVSSMTLSHGYSEINMKNKPGDITIDECVSEFTFGADIDSEFKET 223
QY 212 LSNPLDGYDVSM-----MEPGDAFYVAPPAD-----DMDYVLGVFMESGEADL 254
DB 224 LYSODEHNIVYSNDLEVAAGLVEIQOEFQNLGSANNEMI FDEMDFWFDVLARTGGEQDL 281

RESULT 3
US-10-953-349-22502
; Sequence 22502, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22502
; LENGTH: 275
; TYPE: PRP
; ORGANISM: Glycine max
US-10-953-349-22502

Query Match 48.1%; Score 658; DB 6; Length 275;
Best Local Similarity 46.6%; Pred. No. 6e-41;
Matches 136; Conservative 34; Mismatches 64; Indels 58; Gaps 6;
QY 1 MGRAPCCCKMGLKGPWTPBEDKVLVAHIQRHGNMRAIPKQAGLLRCCKSCRLRWINY 60
DB 1 MVRAPCCCKMGLKGPWAPBEDQILTSYIDKHGHNRAIPKQAGLLRCCKSCRLRWINY 60

QY 61 LRPDIRKGNFSEEDTIIHLHLLGNRWSAIAARLPGRTDNEIKVMWHTLKKRLDAPA 120
DB 61 LRPDIRKGNFTKEEDTIIKLHMLGNRWSAIAAKLPGRDNEIKVMWHTLKKRLD- 116
QY 121 QGGHVAASGGKHKHKKPKSAKPPAAAAAPPASPERSSSVTSSMASSVAEEHGNAGIS 180
DB 117 -----LKSQDSKSKPSKRAIKP-KIERDSNS---SITQSEPDWPNFREM 160
QY 181 SASASYCAKESSFTSA-----SEFQ-----IDSPMSET----- 211
DB 161 TTSSACTTSSSDFSVTVDGSKNIKISBDETETPVIDESFWSAAI DDEPTWSSSQ 220
QY 212 -----LSMPLDGYDVSMERGAFAVAPPADDMYVLGVFMESGEADL 254
DB 221 SLTISNEMRLQYFPANYEETFOGHHAYVSNDDGDWFDYDITRINDSIEL 272

RESULT 4
US-10-953-349-22501
; Sequence 22501, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22501
; LENGTH: 320
; TYPE: PRP
; ORGANISM: Glycine max
US-10-953-349-22501

Query Match 48.1%; Score 658; DB 6; Length 320;
Best Local Similarity 46.6%; Pred. No. 7.1e-41;
Matches 136; Conservative 34; Mismatches 64; Indels 58; Gaps 6;
QY 1 MGRAPCCCKMGLKGPWTPBEDKVLVAHIQRHGNMRAIPKQAGLLRCCKSCRLRWINY 60
DB 46 MVRAPCCCKMGLKGPWAPBEDQILTSYIDKHGHNRAIPKQAGLLRCCKSCRLRWINY 105
QY 61 LRPDIRKGNFSEEDTIIHLHLLGNRWSAIAARLPGRTDNEIKVMWHTLKKRLDAPA 120
DB 106 LRPDIRKGNFTKEEDTIIKLHMLGNRWSAIAAKLPGRDNEIKVMWHTLKKRLD- 161
QY 121 QGGHVAASGGKHKHKKPKSAKPPAAAAAPPASPERSSSVTSSMASSVAEEHGNAGIS 180
DB 162 -----LKSQDSKSKPSKRAIKP-KIERDSNS---SITQSEPDWPNFREM 205
QY 181 SASASYCAKESSFTSA-----SEFQ-----IDSPMSET----- 211
DB 206 TTSSACTTSSSDFSVTVDGSKNIKISBDETETPVIDESFWSAAI DDEPTWSSSQ 265
QY 212 -----LSMPLDGYDVSMERGAFAVAPPADDMYVLGVFMESGEADL 254
DB 266 SLTISNEMRLQYFPANYEETFOGHHAYVSNDDGDWFDYDITRINDSIEL 317

RESULT 5
US-10-953-349-22503
; Sequence 22503, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252


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; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: JP
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39724

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LENGTH: 300
TYPE: PRT
ORGANISM: Oryza sativa
US-10-449-902-33724

Query Match
Best Local Similarity 39.8%; Score 544; DB 6; Length 300;
Matches 118; Conservative 38; Mismatches 66; Indels 36; Gaps 6;

QY 1 MGRAPCCCKMGLKKGPMTPBEDKVLVAHIQRHGHGMRALPKOAGLLRCGKSCRLRWNY 60
DB 1 MGRAPCCCKMGLKKGPMTPBEDKVLVAHIQRHGHGMRALPKOAGLLRCGKSCRLRWNY 60
QY 61 LRPDIKRGNFSKEEDDTIHLHELLGNRWSAIAARLPRTDNEIKYVWTHLKKRL-- 115
DB 61 LRPDIKRGNFSKEEDDTIHLHELLGNRWSAIAARLPRTDNEIKYVWTHLKKRLRMG 120
QY 116 LQAPAGGVAAAGCGKKHKPKAKKPAAPAAAPASPERSASSVTSSMASSVAEEHG 175
DB 121 LDDPPPGPAAGCPAAAHMAQMETARLEAEARLSLSSGVAATTTTAAATTTTSSASSST 180
QY 176 NAGISSASAVCAKESSFTSASEEF-----QIDDSFWSETLSMPLDGYDVMEGDAF 229
DB 181 TGGPVAAAA-----TSPADVFLRLWNSSIGDSF--RKLAVVAAG---SSSPSRAD 225
QY 230 V-----APPSAD 237
DB 226 VTKDAVKQEBEAPAGDD 243

RESULT 9
US-10-449-902-34326
Sequence 34326; Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
TITLE OF INVENTION: Foundation for Advancement of International Science.
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 34326
LENGTH: 266
TYPE: PRT
ORGANISM: Oryza sativa
US-10-449-902-34326

Query Match
Best Local Similarity 38.3%; Score 524; DB 6; Length 266;
Matches 113; Conservative 31; Mismatches 50; Indels 72; Gaps 7;

QY 1 MGRAPCCCKMGLKKGPMTPBEDKVLVAHIQRHGHGMRALPKOAGLLRCGKSCRLRWNY 60
DB 1 MGRAPCCCKMGLKKGPMTPBEDKVLVAHIQRHGHGMRALPKOAGLLRCGKSCRLRWNY 60
QY 61 LRPDIKRGNFSKEEDDTIHLHELLGNRWSAIAARLPRTDNEIKYVWTHLKKRLDA-- 118
DB 61 LRPDIKRGNFSKEEDDTIHLHELLGNRWSAIAARLPRTDNEIKYVWTHLKKRLIARG 120
QY 119 -----PAQGVAAAGCGKKHK-----KPKS 138
DB 121 LDPILTRPLNAAAAVAGHHHLLAAGGSCSPDATSGHSCGDGEYKRGIDILNLSIPSS 180
QY 139 AKPPAAAAAPSPASPS-----ASSSVTSSMASSVAEE-----HG-----MAG 178

DB 181 SSQP-----SSPPPEHEAEARRAGATASYTHHHYSETREKICLCNLHLGHGDECSGC 236
QY 179 ISSASAS-----VCAKESSFTSAS 198
DB 237 GSSASSSSSSPPPATASSRATFANAS 262

RESULT 10
US-10-953-349-33714
Sequence 33714; Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nikolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 33714
LENGTH: 331
TYPE: PRT
ORGANISM: Zea mays subsp. mays
FEATURE:
NAME/KEY: misc feature
LOCATION: (204)..(204)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-953-349-33714

Query Match
Best Local Similarity 38.2%; Score 523; DB 6; Length 331;
Matches 124; Conservative 34; Mismatches 68; Indels 110; Gaps 10;

QY 1 MGRAPCCCKMGLKKGPMTPBEDKVLVAHIQRHGHGMRALPKOAGLLRCGKSCRLRWNY 59
DB 1 MGRAPCCCKMGLKKGPMTPBEDKVLVAHIQRHGHGMRALPKOAGLLRCGKSCRLRWNY 60
QY 60 YLRPDIKRGNFSKEEDDTIHLHELLGNRWSAIAARLPRTDNEIKYVWTHLKKRL-- 116
DB 61 YLRPDIKRGNFSKEEDDTIHLHELLGNRWSAIAARLPRTDNEIKYVWTHLKKRLAAM 120
QY 117 -----DAPAGGVAAAGCGK-----KHKPKS 145
DB 121 GIDPVTYHAKRADVCGSSGAGNNGARVRAAHLSTAQWESARLEAEARLAEARLALA 180
QY 146 AAPAPASP-----ERSASSVTSSMASSVAEE-HG----- 175
DB 181 SPPPPGPGPAPAFSGLSPTSTXSFSESVLPASAAHDHALTSRAVBAFGAEOQORPA 240
QY 176 -----NAGI-----SSASAVCAKESSFTSASEEFQIDDSFW 208
DB 241 DTRAAADAAAPGFLAGVLLGCCSVAGAEKGFASSTDAVLPAPATA 327
QY 209 SETLSWPLDGY-----DVSMEBGDAFVAPSPA 235
DB 292 SSLNWNVSSMSSTSLTSDAVTDPAALVLPAPATA 327

RESULT 11
US-10-449-902-29589
Sequence 29589; Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
TITLE OF INVENTION: Foundation for Advancement of International Science.
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269

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OM protein - protein search, using sw model

Run on: June 24, 2006, 00:04:07 ; Search time 50 Seconds
(without alignments)
449,907 Million cell updates/sec

Title: US-10-521-811-2

Perfect score: 1368

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Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

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7: /EMC_Celerra_SIDS3/ptodata/2/1aa/backfill1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	669.5	48.9	278	1	US-08-722-626B-2 Sequence 2, Appl
2	640	46.8	273	2	US-09-533-029-62 Sequence 62, Appl
3	582	42.5	122	2	US-09-533-029-112 Sequence 112, Appl
4	548	40.1	159	2	US-09-640-211A-2161 Sequence 2161, Appl
5	547.5	40.0	146	2	US-09-640-211A-1110 Sequence 1110, Appl
6	522.5	38.2	412	2	US-09-640-211A-2258 Sequence 2258, Appl
7	506.5	37.0	327	2	US-09-533-029-68 Sequence 68, Appl
8	502	36.7	391	2	US-09-640-211A-2259 Sequence 2259, Appl
9	487	36.3	294	2	US-09-453-387A-2 Sequence 2, Appl
10	495.5	36.2	225	2	US-09-640-211A-2277 Sequence 2277, Appl
11	495	36.2	255	2	US-09-640-211A-2261 Sequence 2261, Appl
12	493	36.0	146	2	US-09-640-211A-2110 Sequence 2110, Appl
13	490	35.8	171	2	US-09-640-211A-2201 Sequence 2201, Appl
14	488.5	35.7	302	2	US-09-453-387A-6 Sequence 6, Appl
15	487	35.6	102	2	US-09-640-211A-872 Sequence 872, Appl
16	483	35.3	176	2	US-09-640-211A-2238 Sequence 2238, Appl
17	483	35.3	371	2	US-09-533-029-86 Sequence 86, Appl
18	481	35.2	269	2	US-09-533-029-94 Sequence 94, Appl
19	476	34.8	144	2	US-09-640-211A-2260 Sequence 2260, Appl
20	475	34.7	205	2	US-09-640-211A-2248 Sequence 2248, Appl
21	471.5	34.5	148	2	US-09-640-211A-1093 Sequence 1093, Appl
22	470	34.4	139	2	US-09-640-211A-1085 Sequence 1085, Appl
23	469.5	34.3	336	2	US-09-533-029-58 Sequence 58, Appl
24	465.5	34.0	192	2	US-09-640-211A-2210 Sequence 2210, Appl
25	465	34.0	414	2	US-09-640-211A-2247 Sequence 2247, Appl
26	463	33.8	153	2	US-09-640-211A-2194 Sequence 2194, Appl

27	459.5	33.6	226	2	US-09-640-211A-2256 Sequence 2256, Appl
28	459	33.6	226	2	US-09-453-387A-4 Sequence 4, Appl
29	456	33.3	126	2	US-09-640-211A-2139 Sequence 2139, Appl
30	450	32.9	107	2	US-09-640-211A-2156 Sequence 2156, Appl
31	450	32.9	107	2	US-09-640-211A-2244 Sequence 2244, Appl
32	449	32.8	107	2	US-09-640-211A-2230 Sequence 2230, Appl
33	445	32.5	113	2	US-09-640-211A-1099 Sequence 1099, Appl
34	440.5	32.2	119	2	US-09-640-211A-1082 Sequence 1082, Appl
35	438	32.0	109	2	US-09-640-211A-2141 Sequence 2141, Appl
36	427	31.2	128	2	US-09-640-211A-1083 Sequence 1083, Appl
37	427	31.2	146	2	US-09-640-211A-2215 Sequence 2215, Appl
38	413.5	30.2	175	2	US-09-640-211A-2159 Sequence 2159, Appl
39	408	29.8	112	2	US-09-640-211A-1112 Sequence 1112, Appl
40	404	29.5	101	2	US-09-640-211A-2169 Sequence 2169, Appl
41	398	29.1	107	2	US-09-640-211A-1118 Sequence 1118, Appl
42	390.5	28.5	208	2	US-09-640-211A-2250 Sequence 2250, Appl
43	390	28.5	148	2	US-09-640-211A-2206 Sequence 2206, Appl
44	387.5	28.3	168	2	US-09-640-211A-2245 Sequence 2245, Appl
45	381	27.9	224	2	US-09-640-211A-919 Sequence 919, Appl

ALIGNMENTS

RESULT 1
US-08-722-626B-2
; Sequence 2, Application US/08722626B
; Patent No. 5939601
; GENERAL INFORMATION:
; APPLICANT: Yang, Yimong
; TITLE OF INVENTION: NOVEL GENES ASSOCIATED WITH ENHANCED
; DISEASE RESISTANCE IN PLANTS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman
; STREET: 1601 Market Street Suite 720
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-2307
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/722,626B
; FILING DATE: 27-SEP-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pat Hagan
; REGISTRATION NUMBER: 27,643
; REFERENCE/DOCKET NUMBER: 97-0010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215 563-4100
; TELEFAX: 215 563-4044
; TELEX:
; INFORMATION FOR SEQ. ID NO. 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 278 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: Internal
; ORIGINAL SOURCE:
; US-08-722-626B-2

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Query Match      48.9%; Score 669.5; DB 1; Length 278;
Best Local Similarity 47.2%; Pred. No. 4.2e-61;
Matches 141; Conservative 37; Mismatches 56; Indels 65; Gaps 10;

QY 1 MGRAPCCCEKMGKKGKGPWTEEDKVLVAHIQRHGHGNWRALPKQAGILRCGKSCRLRWINY 60
DB 1 MGRAPCCCEKMGKKGKGPWTEEDQILISFIQTNGHGNWRALPKQAGILRCGKSCRLRWINY 60
QY 61 LRPDIKRGNFSGKEEDTTIHLHELGNRWSAIAARLPGRTDNEIKXVWHTHLKKRLD-A 118
DB 61 LRPDIKRGNFTKEEBETIIQLHEMLGNRWSAIAAKLPGRTDNEIKXVWHTHLKKRLD-KDYK 120
QY 119 PAGGHNVAASGKKGKPKPS--AKKPAALAA-----APPASPERASASS 160
DB 121 PQO-----NSRRHSKXNDHSGKPTTSSSNSNDLTITNOKAIDSEVLAPNSPQISS 173
QY 161 VTSSSVASVAEEHGNAGISASASVCAKEESFTSASEEF-QIDSPFSETLS----- 213
DB 174 STEMTVTIV-DDH-----QNVYIKQE--VMSSEYFEIDSEFTWDELITDNNMS 221
QY 214 -----MPLDGYDVSNPEGDAPVAPPADMDMYWLGVMESGEADLPQ 256
DB 222 STDHVVAAHQELQVQLPSSSF---KEENVDIATGMEDMDMFVYVVFIKTDLDPELPE 277

RESULT 2
US-09-533-029-62
; Sequence 62, Application US/09533029
; Patent No. 6664446
; GENERAL INFORMATION:
; APPLICANT: Heard, Jacqueline
; APPLICANT: Brown, Pierre
; APPLICANT: Riechmann, Jose-Luis
; APPLICANT: Keddie, James
; APPLICANT: Pineda, Omaira
; APPLICANT: Adam, Luc
; APPLICANT: Samaha, Raymond
; APPLICANT: Zhang, James
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Pilgrim, Marsha
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Reuber, Lynne
; TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES
; FILE REFERENCE: MBI-010
; CURRENT APPLICATION NUMBER: US/09/533,029
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 60/125,814
; EARLIER FILING DATE: 1999-03-23
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 62
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: G233
US-09-533-029-62

Query Match      46.8%; Score 640; DB 2; Length 273;
Best Local Similarity 54.8%; Pred. No. 4.8e-58;
Matches 132; Conservative 19; Mismatches 44; Indels 46; Gaps 4;

QY 1 MGRAPCCCEKMGKKGKGPWTEEDKVLVAHIQRHGHGNWRALPKQAGILRCGKSCRLRWINY 60
DB 1 MGRAPCCCEKMGKKGKGPWTEEDQILISFIQTNGHGNWRALPKQAGILRCGKSCRLRWINY 60
QY 61 LRPDIKRGNFSGKEEDTTIHLHELGNRWSAIAARLPGRTDNEIKXVWHTHLKKRLD-A 120
DB 61 LRPDIKRGNFTKEEBDAIISLHQILGNRWSAIAAKLPGRTDNEIKXVWHTHLKKRLD-DY 119
QY 121 QGGHVAASGKKGKPKPSAKKPAALAAAPPASPERASASSVTSSSVASVAEEHGNAGIS 180
```

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DB 120 QPARKTNKKKGTGPKS-----ESVITSSNSTRESESLABS-----SNPSCGS 163
QY 181 SASASVCAKEESSFTSASEE-----FOIDSPFSET 211
DB 164 LFPSTPSTSEVSMTLISHDGYSNEMNDNKPGRDITIDQECVSFETFGADIDESFWKET 223
QY 212 L 212
DB 224 L 224

RESULT 3
US-09-533-029-112
; Sequence 112, Application US/09533029
; Patent No. 6664446
; GENERAL INFORMATION:
; APPLICANT: Heard, Jacqueline
; APPLICANT: Brown, Pierre
; APPLICANT: Riechmann, Jose-Luis
; APPLICANT: Keddie, James
; APPLICANT: Pineda, Omaira
; APPLICANT: Adam, Luc
; APPLICANT: Samaha, Raymond
; APPLICANT: Zhang, James
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Pilgrim, Marsha
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Reuber, Lynne
; TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES
; FILE REFERENCE: MBI-010
; CURRENT APPLICATION NUMBER: US/09/533,029
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 60/125,814
; EARLIER FILING DATE: 1999-03-23
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 112
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: G241
US-09-533-029-112

Query Match      42.5%; Score 582; DB 2; Length 122;
Best Local Similarity 85.5%; Pred. No. 1.5e-52;
Matches 100; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

QY 1 MGRAPCCCEKMGKKGKGPWTEEDKVLVAHIQRHGHGNWRALPKQAGILRCGKSCRLRWINY 60
DB 1 MGRAPCCCEKMGKKGKGPWTEEDQILISFIQTNGHGNWRALPKQAGILRCGKSCRLRWINY 60
QY 61 LRPDIKRGNFSGKEEDTTIHLHELGNRWSAIAARLPGRTDNEIKXVWHTHLKKRLD 117
DB 61 LRPDIKRGNFTKEEBDAIISLHQILGNRWSAIAAKLPGRTDNEIKXVWHTHLKKRLD 117

RESULT 4
US-09-640-211A-2161
; Sequence 2161, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1021C1U
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
```


Dd 168 DVSRCDDKSSSHVESJLNRET--NHRNLSTSMS-----SGGSNGQDPPXIDELRF 217
 | :

Oy 206 -----SFWSETLSPMLDGVDVSMPCGAFVAAPSADMDWY 241
 ||::||:

Db 218 EYTEEAYSFENDIIIOEVDKPDLLETFPS-----DPDWI 252

```

RESULT 8
US-09-640-211A-2259
: Sequence 2259, Application US/09640211A
: Patent No. 6833446
: GENERAL INFORMATION:
: APPLICANT: Wood, Marion
: APPLICANT: Shenk, Michael A.
: APPLICANT: McGrath, Annette
: APPLICANT: Glenn, Matthew
: TITLE OF INVENTION: Compositions and Methods for the
: FILE REFERENCE: 11000.1021CU
: CURRENT APPLICATION NUMBER: US/09/640,211A
: NUMBER OF SEQ ID NOS: 2368
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 2259
: LENGTH: 391
: TYPE: PRF
: ORGANISM: Pinus radiata
: US-09-640-211A-2259

```

Query Match	36.74%	Score 502	Db 2	Length 391	
Best Local Similarity	41.94%	Pred.	1	De-43	
Matches	108	Conservative	30	Mismatches	84
				Indels	36
				Gaps	6
Qy	1	MGRAPCCCKGKGLKKGPWTBEDKLVLAHIQRHGHGNMRALPKYQAGLLRCGSCSCLRMVINY	60		
Db	1	MGRPPCLTKGILNRGPMWTBEDCLSNYTEAIGEGGMRTLPRKQAGLLRCGSCSCLRMVINY	60		
Qy	61	LRPDIKKNFSKEEEDTIIHLHELGNRMSAIAARLPGRTDIEINVMHTLKKRLDAP-	119		
Db	61	LRPVNRGHTLLPEBEDLIRLHRLGNRSLIAGNMPRTDDEVNVMYHTLSKKLLSOG	120		
Qy	120	-----AQGGHVAASGGKHKHKKYSKKCPAAAAAPPASPEKASASSVTESMASSV	170		
Db	121	IDPRTHKPLSESEDISSPENSESVSRKSORENNAAI-----PRVVAAGVADIODKEEDI	174		
Qy	171	AEEHGNAGIS-----SASASVCAKEESSFT-----SASEFOIDDSFMSEITLSP----	215		
Db	175	TEBQTSAGLPEENQLLETFSNQCPSVATDVPQAPSPISAFYSFO-----QSTTSVFGV	229		
Qy	216	LDGIVDSMERGDPAFVAP	233		
Db	230	SDSVDVVHNKGSKVPPFP	247		

```

RESULT 9
US-09-453-387A-2
: Sequence 2, Application US/09453387A
: Patent No. 6828675
:
: GENERAL INFORMATION:
: APPLICANT: Wilkins, Thea A.
: TITLE OF INVENTION: The Regents of the University of California
: FILE REFERENCE: 023070-095600US
: CURRENT APPLICATION NUMBER: US/09/453,387A
: CURRENT FILING DATE: 1999-12-02
: NUMBER OF SEQ ID NOS: 26
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 2
:
: LENGTH: 294
:
: TYPE: PRT
: ORGANISM: Goseyptium hirsutum
: US-09-453-387A-2

```

Query Match	36.3%	Score 497;	DB 2;	Length 294;
Best Local Similarity	43.3%	Pred. No. 3,9e-43;		
Matches	104;	Conservative	43;	Mismatches 77; Indels 16; Gaps 4

QY	1	MGRAPCCGKMLKGPWTPEEDKVLVAHIQRHGHGNFALPKQAGLLRGKSCRLRWY	60
DB	1	MGRSPCEKATNTNGAMTKEDDRLINIVRHGECMSLPLQAGLLRGKSCRLRWY	60
QY	61	LRPDIKRGNFSEKEEDTIIHLHELLGNWSAIIAARLPRTDNEIGNVHTHLKKRLDAPA	120
DB	61	LRPDLKGNFTFEEDELLIKHLSLGNKSLIAGLPPRTDNEIGNVHTHLKKRL----	116
QY	121	QGGHVAASGGKHKHKPKSAKPPAAAAAAPSPASPERSASSVTSESSMASSVAEHNAGIS	180
DB	117	-----ISRIGIDQTHRLPLNTANTNTVTVAPELDFENSPSVSKSSIKNPISLDF--NYNEF	171
QY	181	SASASVACKESSESTPSA-----EEFOIDDSFWSSETLMPDGYGVSWMPGDAFAVAPPA	235
DB	172	QFKSTSDLEBPNTCTASSGMMTTDEEQ--EQHKKQGYGSPSGQDINLELSIGIYSABDS	229

```

RESULT 10
US-09-640-211A-2277
; Sequence 2277, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Modification of Gene Transcription
; FILE REFERENCE: 11000.1021C1U
; CURRENT APPLICATION NUMBER: US/09/640.211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2277
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Pinus radiata
US-09-640-211A-2277

```

	Query Match	Similarity	Score	DB 2:	Length	225;
	Best Local	Similarity	50.5%	Pred.	No.3.7e-43;	
	Matches	97; Conservative	27;	Mismatches	51;	Indels 17; Gaps 4
QY	1	MGRAPCCCKMYLKKGPWTPREEDKVLVAHIIORHGHNMBALPKOAGILRSGKSCLRWINY	60			
D8	1	MGRSPCEKAHTNKGAWTKEODDLIAHIRAHGEGGSLSLPXAGILRGSKSCRLRWINY	60			
QY	61	LRPDIKRGNESKEBEDTITIHHELLGNWSAIAALTERTONEIKNWNTTHLKRYLDAPA	120			
D8	61	LRPDIKRGPSFEEBEDELTIKLHSFGNWSLSIAGLRPGTDNEIKYWMTTHIKRKLLSNG	120			
QY	121	OQGHVAAOSGGKHKKKPSAKKPRAAAAAR---PASPE-----RSASSSVTSMSAS	168			
D8	121	LDPOTHRIRLGQRNMTP--VTNRVLDEHRIFAFONPATPRTELADLIQHNRLESSPI---KPAH	175			
QY	169	SVAEBHGNAGIS 180				
D8	176	SDAEENHPDNLIN 187				

```

RESULT 11
US-09-640-211A-2261
; Sequence 2261, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shank, Michael A.
; APPLICANT: McGrath, Annette

```


APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Compositions and Methods for the
FILE REFERENCE: 11000.1021CIU
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2261
LENGTH: 255
TYPE: PRT
ORGANISM: Pinus radiata
US-09-640-211A-2261

Query Match 36.2%; Score 495; DB 2; Length 255;
Best Local Similarity 46.0%; Pred. No. 5.1e-43;
Matches 103; Conservative 28; Mismatches 65; Indels 28; Gaps 3;

1 MGRAPCEKMKLKGKMPTEEDKVLVAH1QRHGHGMRALPKOAGLLRCGSKRLRWINY 60
1 MGRSPCEKMTNKGAVTKEEDRLIAH1RTHGEGCRSLPKAAGLLRCGSKRLRWINY 60
61 LRPD1KRGNFSEEDTIIHLHLLGNRWSA1AARLPGRDNEIKVWHTLKKRLDAPA 120
61 LRDLKRGNFSEEDDELIVIKLHSLGNKWSL1AGRLPGRTDNEIKVWHTHIKRLINRG 120
121 OGGHVAASGGKKGKPKSA-----KKPAAAAAPPASPERASSSVTESSMA 167
121 LPEQSHRPLQPHNSNTCPSPALPEHEILVFORPRTPEIADPFQYERSESSPMEPAT-- 178
168 SSVAEHGNAGI-----SSASAVCAKESSFTSAS 198
179 SKDAEHPDLNLCISLPVHSPATSRASSVDGTQVSKNSVS 222

RESULT 12

US-09-640-211A-2110
Sequence 2110, Application US/09640211A
Patent No. 6833446
GENERAL INFORMATION:
APPLICANT: Wood, Marion
APPLICANT: Shenk, Michael A.
APPLICANT: McGrath, Annette
APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Compositions and Methods for the
FILE REFERENCE: 11000.1021CIU
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2110
LENGTH: 146
TYPE: PRT
ORGANISM: Eucalyptus grandis
US-09-640-211A-2110

Query Match 36.0%; Score 493; DB 2; Length 146;
Best Local Similarity 64.1%; Pred. No. 3.6e-43;
Matches 93; Conservative 14; Mismatches 24; Indels 14; Gaps 2;

6 CCEKMGKKGKMPTEEDKVLVAH1QRHGHGMRALPKOAGLLRCGSKRLRWINYLRPD1 65
1 CCEKMGKKGKMPTEEDKVLVAH1QRHGHGMRALPKOAGLLRCGSKRLRWINYLRPD1 60
66 KRGNFSEEDTIIHLHLLGNRWSA1AARLPGRDNEIKVWHTLKKRLDAPA 116
61 KRGNFSEEDTIIHLHLLGNRWSA1AARLPGRDNEIKVWHTLKKRLDAPA 120
117 DAPAGHVAASGGKKGKPKSA 141
121 HKPKNDALVSSDG-----OSKSAK 140

RESULT 13
US-09-640-211A-2201
Sequence 2201, Application US/09640211A
Patent No. 6833446
GENERAL INFORMATION:
APPLICANT: Wood, Marion
APPLICANT: Shenk, Michael A.
APPLICANT: McGrath, Annette
APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Compositions and Methods for the
FILE REFERENCE: 11000.1021CIU
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2201
LENGTH: 171
TYPE: PRT
ORGANISM: Eucalyptus grandis
US-09-640-211A-2201

Query Match 35.8%; Score 490; DB 2; Length 171;
Best Local Similarity 72.0%; Pred. No. 9.2e-43;
Matches 85; Conservative 16; Mismatches 17; Indels 0; Gaps 0;

1 MGRAPCEKMKLKGKMPTEEDKVLVAH1QRHGHGMRALPKOAGLLRCGSKRLRWINY 60
1 MGRSPCEKMTNKGAVTKEEDRLIAH1RTHGEGCRSLPKAAGLLRCGSKRLRWINY 60
61 LRPD1KRGNFSEEDTIIHLHLLGNRWSA1AARLPGRDNEIKVWHTLKKRLDAPA 118
61 LRDLKRGNFSEEDDELIVIKLHSLGNKWSL1AGRLPGRTDNEIKVWHTHIKRLDAPA 118

RESULT 14

US-09-453-387A-6
Sequence 6, Application US/09453387A
Patent No. 6828476
GENERAL INFORMATION:
APPLICANT: Wilkins, Thea A.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Cotton Transcription Factors and Their Uses
FILE REFERENCE: 023070-095600US
CURRENT APPLICATION NUMBER: US/09/453,387A
CURRENT FILING DATE: 1999-12-02
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 302
TYPE: PRT
ORGANISM: Gossypium hirsutum
US-09-453-387A-6

Query Match 35.7%; Score 488.5; DB 2; Length 302;
Best Local Similarity 41.3%; Pred. No. 3.1e-42;
Matches 112; Conservative 38; Mismatches 84; Indels 37; Gaps 8;

1 MGRAPCEKMKLKGKMPTEEDKVLVAH1QRHGHGMRALPKOAGLLRCGSKRLRWINY 60
1 MGRSPCEKMTNKGAVTKEEDRLIAH1RTHGEGCRSLPKAAGLLRCGSKRLRWINY 60
61 LRPD1KRGNFSEEDTIIHLHLLGNRWSA1AARLPGRDNEIKVWHTLKKRLDAPA 120
61 LRDLKRGNFSEEDDELIVIKLHSLGNKWSL1AGRLPGRTDNEIKVWHTHIKRLDAPA 119
121 OGGHVAASGGKKGKPKSA-----KKPAAAAAPPASPERASSSVTESSMA----- 167
120 QNSPAAPS-----KNDEAARGRTAGNGNTNGSGSSSTHVTRTRATRCSTKVFINPHYT 174
168 -----SSVAEHN-----AGISSASAVCAKESSFTS--ASEFQIDDSFMSSETLS-- 213

Db 175 QNRDPKRSSTCSNHDHREPKTMNELLPIMSESENEGTTDHISSDFTDFNMGEFCLSD 234

QY 214 -MPLDGYDVS-MEPGDAFVAFPSADD-MDY 240

Db 235 LNSDFCDVNEMLNYSNGFDSFSPDQPPMDF 265

RESULT 15

US-09-640-211A-872

; Sequence 872, Application US/09640211A

; Patent No. 6833446

; GENERAL INFORMATION:

; APPLICANT: Wood, Marion

; APPLICANT: Shenk, Michael A.

; APPLICANT: McGrath, Annette

; APPLICANT: Glenn, Matthew

; TITLE OF INVENTION: Compositions and Methods for the

; FILE REFERENCE: 11000.1021CIU

; CURRENT APPLICATION NUMBER: US/09/640,211A

; CURRENT FILING DATE: 2000-08-16

; NUMBER OF SEQ ID NOS: 2368

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 872

; LENGTH: 102

; TYPE: PRT

; ORGANISM: Eucalyptus grandis

US-09-640-211A-872

Query Match 35.6%; Score 487; DB 2; Length 102;

Best Local Similarity 79.4%; Pred. No. 8.8e-43; Mismatches 8; Indels 0; Gaps 0;

Matches 81; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

QY 1 MGRAPCCCEKMGKGPWTPEBDKVLVAHIOHGHGWRALPKQAGLLRCGKSCRLRWINY 60

Db 1 MATTPCCCEKMGKGPWTPEBDQILSHIQFHSNWRALPRQAGLLRCGKSCRLRWINY 60

QY 61 LRPDIKRGNFSKEEDTIIHHELLGNRMSAIAARLPGRITDN 102

Db 61 LRPDVTRKGNFTDDEDTIIELHQLVGNRMSAIAARLPGRITDN 102

Search completed: June 24, 2006, 00:05:31
Job time : 51 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 23, 2006, 23:55:27 ; Search time 296 Seconds
(without alignments)
803.139 Million cell updates/sec

Title: US-10-521-811-2
Perfect score: 1368
Sequence: 1 MGRAPCCRCMKGLKGPWTPPE.....MDYMLGVPMESGAQDLPGI 257

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 7.2.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1368	100.0	257	MYB4_ORYSA	Q7XBH4_oryza_sativ
2	933	68.2	277	061X77_WHEAT	061X77_triticum_ae
3	835.5	61.1	288	096463_HORVU	096463_hordeum_vul
4	827.5	60.5	258	06K186_ORYSA	06K186_oryza_sativ
5	709.5	51.9	280	002993_PETTY	002993_petunia_hyb
6	697.5	51.0	276	004108_ORYSA	004108_oryza_sativ
7	697.5	51.0	276	07XDC7_ORYSA	07XDC7_oryza_sativ
8	694	50.7	281	09SLT0_TOBAC	09SLT0_nicotiana_t
9	690	50.4	281	09SLT2_TOBAC	09SLT2_nicotiana_t
10	687	50.2	265	040174_LYCES	040174_lycopersico
11	684	50.0	277	09SLT1_TOBAC	09SLT1_nicotiana_t
12	677.5	49.5	264	09SLT3_SOYBN	09SLT3_glycine_max
13	669.5	48.9	278	P93391_TOBAC	P93391_nicotiana_t
14	665.5	48.6	262	09XIU9_SOYBN	09XIU9_glycine_max
15	661.5	48.4	285	09LTC4_ARYTH	09LTC4_arabidopsis
16	658	48.1	275	09XIU8_SOYBN	09XIU8_glycine_max
17	653.5	47.8	253	08LSN7_9ROSI	08LSN7_vitis_labru
18	648.5	47.4	270	02LME1_MALDO	02LME1_malus_domes
19	646.5	47.3	253	08LSN8_9ROSI	08LSN8_vitis_labru
20	646	47.2	233	02VOV6_DAUCA	02VOV6_daucus_caro
21	645.5	47.2	232	09XIU5_SOYBN	09XIU5_glycine_max
22	640	46.8	273	049744_ARYTH	049744_arabidopsis
23	628.5	45.9	246	09LNC9_ARYTH	09LNC9_arabidopsis
24	623.5	45.6	246	039153_ARYTH	039153_arabidopsis
25	608	44.4	249	09SLX8_ARYTH	09SLX8_arabidopsis
26	595	43.5	157	06OD72_NICBE	06OD72_nicotiana_b
27	585.5	42.8	340	06YU06_ORYSA	06YU06_oryza_sativ
28	582	42.5	122	039260_ARYTH	039260_arabidopsis
29	576	42.1	345	07XUV5_ORYSA	07XUV5_oryza_sativ
30	568	41.5	371	07X793_ORYSA	07X793_oryza_sativ
31	563.5	41.2	340	MYB1_MAIZE	P20024_zea_mays (m

32	562	41.1	274	2	Q9SA47_ARYTH	Q9SA47_arabidopsis
33	561	41.0	272	2	Q8LE55_ARYTH	Q8LE55_arabidopsis
34	550.5	40.2	357	2	Q8GUA1_ORYSA	Q8GUA1_oryza_sativ
35	550	40.2	368	2	004141_ORYSA	004141_oryza_sativ
36	549	40.1	368	2	06Z414_ORYSA	06Z414_oryza_sativ
37	546	39.9	299	2	Q9M2D9_ARYTH	Q9M2D9_arabidopsis
38	546	39.9	300	2	06H7S0_ORYTH	06H7S0_oryza_sativ
39	544	39.8	267	2	0652E6_ORYSA	0652E6_oryza_sativ
40	543	39.7	110	2	084XW1_LOUPR	084XW1_lolium_pere
41	541.5	39.6	367	2	Q84U53_9ASPA	Q84U53_dendrobium
42	533	39.0	294	2	Q6R0A6_ARYTH	Q6R0A6_arabidopsis
43	532	38.9	325	2	Q6R054_ARYTH	Q6R054_arabidopsis
44	532	38.9	325	2	Q9LPE1_ARYTH	Q9LPE1_arabidopsis
45	532	38.9	336	2	Q84PP4_LOUTJA	Q84PP4_lotus_japon

ALIGNMENTS

RESULT 1
ID MYB4_ORYSA STANDARD; PRT; 257 AA.
AC Q7XBH4; O04140; Q7XKW3; Q8SA75;
DT 30-AUG-2005, Integrated into UniprotKB/Swiss-Prot.
DT 30-AUG-2005, sequence version 2.
DT 07-MAR-2006, entry version 21.
DE Myb-related protein Myb4 (OemMyb4) (Transcription factor RLTR1).
GN Name=MYB4; Synonyms=LTRL; OrderedLocustNames=Os04g43680;
GN ORFNames=OSUNBA0073E02.6;
OX Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
OC Eriartoideae; Oryzaeae; Oryza.
OX NCBI_TaxId=4530;
[1]
NP NUCLEOTIDE SEQUENCE [MRNA], AND INDUCTION.
RC STRAIN=cv. Japonica / Arborio; TISSUE=coleoptile;
RA Pandolfi D., Solinas G., Valle G., Coraggio I.;
RT "Cloning of a cDNA encoding a novel myb gene highly expressed in cold
RT stressed rice coleoptiles";
RL (er) Plant Gene Register PCR97-079.
[2]
NP NUCLEOTIDE SEQUENCE [MRNA].
RC STRAIN=cv. Japonica;
RA Quanhong Y., Rhee P., Aisheng X.;
RT "MYB-family protein acts as a signal transporter in JA induced
RT resistance";
RN Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
[3]
NP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=cv. Japonica / Nipponbare;
RX MEDLINE=22337377; PubMed=12447439; DOI=10.1038/nature01183;
RA Feng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J.,
RA Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,
RA Wang X., Zhang L., Lu Y., Mu J., Lu Y., Zhang L.S., Hu H., Guan D.,
RA Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,
RA Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H.,
CAI Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y.,
RA Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W.,
RA Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,
RA Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
RA Han B.;
RT "Sequence and analysis of rice chromosome 4.";
RL Nature 420:316-320(2002).
[4]
NP NUCLEOTIDE SEQUENCE [MRNA] OF 1-159.
RA Yao Q., Peng R., Xiong A., Li X., Fan H.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
[5]
NP FUNCTION, AND INDUCTION.
RX PubMed=14675437; DOI=10.1046/j.1365-313X.2003.01938.x;
RA Vannini C., Locatelli F., Bracale M., Magnani E., Marsoni M.,
RA Osnato M., Mattana M., Baldoni E., Coraggio I.;

```

RT "Overexpression of the rice Osmyl4 gene increases chilling and
RT freezing tolerance of Arabidopsis thaliana plants."
RL Plant J. 37:115-127(2004).
CC -1- FUNCTION: Putative transcription factor which is may be involved
CC in cold stress response.
CC -1- SUBCELLULAR LOCATION: Nucleus (Probable).
CC -1- INDUCTION: By cold stress.
CC -1- MISCELLANEOUS: Arabidopsis plants overexpressing MYB4 show dwarf
CC phenotype and increased tolerance to cold and freezing.
CC -1- SIMILARITY: Contains 2 Myb DNA-binding domains.
CC -1- CAUTION: Ref.4 sequence differs from that shown due to a
CC frameshift in position 138.
-----
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CC
DR EMBL, Y11414; CAA72217.1; -; mRNA.
DR EMBL, AY323484; AAP92750.1; -; mRNA.
DR EMBL, AL731616; CAE05446.2; -; Genomic DNA.
DR EMBL, AF467733; AAL78372.1; ALT_FRAME; mRNA.
DR PIR, T03825; T03825.
DR HSSP, P06876; 1GVZ.
DR Gramene; Q7XBH4; -.
DR InterPro; IPR001005; Myb DNA bd.
DR Pfam; PF00249; Myb DNA-binding; 2.
DR SMART, SM00717; SANT; 2.
DR PROSITE, PS00037; MYB_1; 1.
DR PROSITE, PS00334; MYB_2; 1.
DR PROSITE, PS50090; MYB_3; 2.
DR KMW, DNA-binding; Nuclear protein; Transcription; Transcription regulation.
FT CHAIN 1 257 /FTid=PRO_0000197080.
FT DNA_BIND 9 61 Myb 1.
FT DNA_BIND 62 112 Myb 2.
FT CONFLICT 138 159 SAKKPAAPAAAPPASPERSSASS -> TRRSQPPPPRGVA
FT CONFLICT 152 152 S -> L (in Ref. 2).
FT CONFLICT 257 AA; 27914 MW; E2B602B89FC9BC37 CRC64;
SQ SEQUENCE 257 AA; 27914 MW; E2B602B89FC9BC37 CRC64;

Query Match 100.0%; Score 1368; DB 1; Length 257;
Best Local Similarity 100.0%; Pred. No. 2.5e-93;
Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRAPCCCEKMGKKGWPTPEEDKVLVAHIQRHGHGNWRALPKOAGILRCGKSCRLRWINY 60
DB 1 MGRAPCCCEKMGKKGWPTPEEDKVLVAHIQRHGHGNWRALPKOAGILRCGKSCRLRWINY 60
QY 61 LRPDIKRGNFSEEDTIIHLHELGNRWSAIAARLPGRTDNEIKVWHTHLKKRLDAPA 120
DB 61 LRPDIKRGNFSEEDTIIHLHELGNRWSAIAARLPGRTDNEIKVWHTHLKKRLDAPA 120
QY 121 OGCHVAASGGKGGKKPKAKKPAAPASPERASSSVTESSMAASVAEHHGAGIS 180
DB 121 OGCHVAASGGKGGKKPKAKKPAAPASPERASSSVTESSMAASVAEHHGAGIS 180
QY 121 OGCHVAASGGKGGKKPKAKKPAAPASPERASSSVTESSMAASVAEHHGAGIS 180
DB 121 OGCHVAASGGKGGKKPKAKKPAAPASPERASSSVTESSMAASVAEHHGAGIS 180
QY 181 SASASVCAKESSFTSASEEFOIDSFWSSETLMPIDGYDVMEPDAFVAPPSADMDY 240
DB 181 SASASVCAKESSFTSASEEFOIDSFWSSETLMPIDGYDVMEPDAFVAPPSADMDY 240
QY 241 WLGVMESEGAODLPQI 257
DB 241 WLGVMESEGAODLPQI 257

RESULT 2
Q6IX77 WHEAT PRELIMINARY; PRT; 277 AA.
AC Q6IX77.
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE Transcription factor Myb2.
GN Name=Myb2;

```

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OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
OC Poideae; Triticeae; Triticum.
OX NCBI_TaxId=4565;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Seed.
RA Chen R., Ni Z., Sun Q.;
RL Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Nucleus (By similarity).
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CC
DR EMBL, AY615199; AAT37168.1; -; mRNA.
DR HSSP, Q03237; 1ASJ.
DR Gramene; Q6IX77; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0045448; P:regulation of transcription; IEA.
DR InterPro; IPR012287; Homeodomain-rel.
DR InterPro; IPR010005; Myb DNA bd.
DR Pfam; PF00249; Myb DNA-binding; 2.
DR SMART, SM00717; SANT; 2.
DR PROSITE, PS00037; MYB_1; UNKNOWN_1.
DR PROSITE, PS00334; MYB_2; 1.
DR PROSITE, PS50090; MYB_3; 2.
DR KMW, DNA-binding; Nuclear protein; Repeat.
SQ SEQUENCE 277 AA; 30633 MW; D66F95B71EADAE9 CRC64;

Query Match 68.2%; Score 933; DB 2; Length 277;
Best Local Similarity 69.6%; Pred. No. 4.9e-61;
Matches 195; Conservative 16; Mismatches 43; Indels 26; Gaps 9;

QY 1 MGRAPCCCEKMGKKGWPTPEEDKVLVAHIQRHGHGNWRALPKOAGILRCGKSCRLRWINY 60
DB 1 MGRAPCCCEKMGKKGWPTPEEDKVLVAHIQRHGHGNWRALPKOAGILRCGKSCRLRWINY 60
QY 61 LRPDIKRGNFSEEDTIIHLHELGNRWSAIAARLPGRTDNEIKVWHTHLKKRLDAPA 120
DB 61 LRPDIKRGNFSEEDTIIHLHELGNRWSAIAARLPGRTDNEIKVWHTHLKKRLDAPA 120
QY 121 OGCHVAASGGKGGKKPKAKKPAAPASPERASSSVTESSMA 167
DB 121 OGCHVAASGGKGGKKPKAKKPAAPASPERASSSVTESSMA 167
QY 168 SSVAAE-HGNAGISSASASVCAKESSFTSA--SEFQIDSFWSSETLMPIDGY-DVSN 223
DB 168 SSVAAE-HGNAGISSASASVCAKESSFTSA--SEFQIDSFWSSETLMPIDGY-DVSN 223
QY 181 ASAAEEHGNNG-SASASASVKEE-CFTSSESEEFQIDSEFWSETLSTPDDINDVCM 238
DB 181 ASAAEEHGNNG-SASASASVKEE-CFTSSESEEFQIDSEFWSETLSTPDDINDVCM 238
QY 224 EPGDAFVAPPSADMDYWLGVMESEGAODLPQI 257
DB 224 EPGDAFVAPPSADMDYWLGVMESEGAODLPQI 257
QY 239 EPHDAF-GKPADGDMYWLKVMGEGDDNDGALDLPQI 277
DB 239 EPHDAF-GKPADGDMYWLKVMGEGDDNDGALDLPQI 277

RESULT 3
Q96463 HORVU PRELIMINARY; PRT; 288 AA.
AC Q96463.
DT 01-FEB-1997, integrated into UniProtKB/TrEMBL.
DT 01-FEB-1997, sequence version 1.
DT 07-FEB-2006, entry version 32.
DE Myb4 transcription factor (Fragment).
GN Name=Myb4;
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
OC Poideae; Triticeae; Hordeum.
OX NCBI_TaxId=4513;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Endosperm;

```

RA Gubler F., Roberts J.K., Jacobsen J.;
 RT "Cloning of a cDNA Encoding a Nobel Myb Expressed in Barley Aleurone
 RL Layer" (Accession X99973) (G897-013)";
 CC Plant Physiol. 113:306-306(1997).
 CC -----
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 CC -----
 DR EMBL, X99973; CAA68235.1; -; mRNA.
 DR F01, T05954; T05954.
 DR HSP, P06876; 1MBK.
 DR Gramine; Q96463; -.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0045449; P:regulation of transcription; IEA.
 DR InterPro; IPR012287; Homeodomain-rel.
 DR InterPro; IPR012287; Homeodomain-rel.
 DR Pfam; PF00249; Myb DNA-binding; 2.
 DR SMART; SM00717; SANT; 2.
 DR PROSITE; PS00334; MYB_2; 1.
 DR PROSITE; PS50090; MYB_3; 2.
 DR Nuclear protein.
 FT NON_TER
 SQ SEQUENCE 288 AA; 31044 MW; 40BE589A9C5F7D38 CRC64;
 Query Match 61.1%; Score 835.5; DB 2; Length 288;
 Best Local Similarity 64.7%; Pred. No. 8; 7e-54;
 Matches 180; Conservative 12; Mismatches 47; Indels 39; Gaps 7;
 QY 16 PWTPEDEVVAHQHGHGHWRLPKQAGLLRCGKSCRLRWINTYRDIKGNFSEKEE 75
 DB 14 PVDAAECKLVHSHGHGHWRLPKQAGLLRCGKSCRLRWINTYRDIKGNFSEKEE 73
 QY 76 DTIIHLHELGNRMSAIAARLPGRDNEIKVWHTLKKRLDPAQGGHVAASGGKXKK 135
 DB 74 OSIILHQLGNRMSAIAARLPGRDNEIKVWHTLKKRLDPAQGGHVAASGGKXKK 133
 QY 136 PMSAK-----KPAASAAAPASPERSSASSVTESSMASSVAEHN 176
 DB 134 PAAASAAAPKRDGCKVKNRNALNTARAAAPASPERSSASSVTESSMASSVAEHN 193
 QY 177 AGISSASASVCAKESSFTSA--SEEFQIDSFWSSTLSMPLDGY-DVSMERQDAFVAP 233
 DB 194 SGSSASASASVKEE-CFTSSSESEEFQIDSFWSSTLSMPLDLDVCMERHDAFGKRD 252
 QY 234 SADDMDYLVGFMESE-----EAQDLPOI 257
 DB 253 G--DMDYVLRFLFMEGGSGSGSGSDNNHHDGALDLPQI 288
 RESULT 4
 Q6K1S6_ORYSA PRELIMINARY; PRT; 258 AA.
 AC Q6K1S6;
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 07-FEB-2006, entry version 18.
 DE Putative myb protein.
 GN Name=B1215B07.15;
 OS Oryza sativa (Japonica cultivar-group).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BPP clade;
 CC Eriocaridaceae; Oryzaceae; Oryza.
 CC NCBI_TaxID=39947;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Sasaki T., Matsumoto T., Katayose Y.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
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 CC -----

DR EMBL, AF006523; BAD23776.1; -; Genomic_DNA.
 DR HSP, Q03237; 1A5J.
 DR Gramine; Q6K1S6; -.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0045449; P:regulation of transcription; IEA.
 DR InterPro; IPR012287; Homeodomain-rel.
 DR InterPro; IPR012287; Homeodomain-rel.
 DR Pfam; PF00249; Myb DNA-binding; 2.
 DR SMART; SM00717; SANT; 2.
 DR PROSITE; PS00334; MYB_2; UNKNOWN_1.
 DR PROSITE; PS00334; MYB_2; 1.
 DR PROSITE; PS50090; MYB_3; 2.
 DR DNA-binding; Nuclear protein; Repeat.
 SQ SEQUENCE 258 AA; 28469 MW; 61FDB01C586612EB CRC64;
 Query Match 60.5%; Score 827.5; DB 2; Length 258;
 Best Local Similarity 62.1%; Pred. No. 3e-53;
 Matches 169; Conservative 29; Mismatches 45; Indels 29; Gaps 8;
 QY 1 MGRAPCCCKKGLKKGWTEBEDKVVAHQHGHGHWRLPKQAGLLRCGKSCRLRWINTY 60
 DB 1 MGRAPCCCKKGLKKGWTEBEDKVVAHQHGHGHWRLPKQAGLLRCGKSCRLRWINTY 60
 QY 61 LRPDIKGNFSEKEEDTIIHLHELGNRMSAIAARLPGRDNEIKVWHTLKKRLDAPA 120
 DB 61 LRPDIKGNFSEKEEDTIIHLHELGNRMSAIAARLPGRDNEIKVWHTLKKRLDAPA 120
 QY 121 OGSHVAASGKXKKKPKAKKAPAAAAA-----PPASPERSSASSVTESSMASSVAE 174
 DB 121 SGSEKAAA-----PKKATKKAQAAVAVADVPTTVSESGSISTTTT--SAATTEEV 171
 QY 175 GNAGISASASVCAKESSFTSA--SEEFQIDSFWSSTLSMPLDGYVNE-----PGDA 229
 DB 172 SYSMASSADHNT-----TDSFTS--SEEFQIDSFWSSTLSMPLDGYVNE-----PGDA 226
 QY 230 VAPPSA--DDM-DYLVGFMESEGAQDLPOI 257
 DB 227 GASPPSSNDMDDFWLKLFIOAGGMONLPQI 258
 RESULT 5
 Q02993_PETHY PRELIMINARY; PRT; 280 AA.
 AC Q02993;
 DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
 DT 07-FEB-2006, entry version 37.
 DE Protein 2.
 GN Name=myb.ph2;
 OS Eucarya; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 CC asterids; lamiales; Solanales; Solanaceae; Petunia.
 CC NCBI_TaxID=4102;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=V26; TISSUE=Floral;
 RC MEDLINE=94035159; PubMed=8220462;
 RA Avila J., Nieto C., Canas L., Benito M.J., Paz-Ares J.;
 RT "Petunia hybrida genes related to the maize regulatory C1 gene and to
 RT animal myb proto-oncogenes";
 RL Plant J. 3:553-562(1993).
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
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 CC -----
 DR EMBL, Z13997; CAA78387.1; -; mRNA.
 DR F01, S26604; S26604.
 DR HSP, P06876; 1GV2.
 DR TRANSFAC; T02890; -.
 DR GO; GO:0005634; C:nucleus; IEA.

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DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0045449; F:regulation of transcription; IEA.
DR InterPro; IPR012287; Homodomain-rel.
DR InterPro; IPR01005; MYB_DNA_Bd.
DR Pfam; PF00249; MYB_DNA-binding; 2.
DR SMART; SM00717; SANT; 2.
DR PROSITE; PS00037; MYB_1; UNKNOWN_1.
DR PROSITE; PS00334; MYB_2; 1.
DR PROSITE; PS00390; MYB_3; 2.
DR DNA-binding; Nuclear protein; Repeat.
SQ SEQUENCE 280 AA; 32178 MW; 2A687374F02C25F4 CRC64;

Query Match 51.9%; Score 709.5; DB 2; Length 280;
Best Local Similarity 50.5%; Pred. No. 1.9e-44;
Matches 149; Conservative 36; Mismatches 55; Indels 55; Gaps 10;

QY 1 MGRAPCCCKMGLKKGPMTPPEEDKVLVAHIQRHGHGNWRALPKOAGILRCGSKCRLRWNY 60
DB 1 MGRAPCCCKMGLKKGPMTPPEEDKVLVAHIQRHGHGNWRALPKOAGILRCGSKCRLRWNY 60
QY 61 LRPDIKRGNFSEEDDTIHLHELLGNRWSAIAARLPGRTDNEIKVWHTLKKRLD--A 118
DB 61 LRPDIKRGNFSEEDDTIHLHELLGNRWSAIAARLPGRTDNEIKVWHTLKKRLD--A 120
QY 119 PAQGGHVAASGGKKGKKPKSAK-----KPAATAAPASPERSA--SSS 160
DB 121 PPOASKRHSKNNHDSKAPSTSKMLNDSBSFTIOENINPMTG---PNSPORSSESST 176
QY 161 VTSSMASSVAEHNAGISASASVCAKESSFTSASEF-QIDDSFWSETLSMPLDGY 219
DB 177 VTADSLAAT-----DVTNDQTFIKHE--MDSYENFPEIDESFWTDLDSMG-DWL 224
QY 220 DVSME-PGDA-----PAAPSADMDYWLGVFMESGEGADLPQ 256
DB 225 DLDMEVAGEKQVQPPYSHDKQGVDMVGAKLEDMDMFWYVFTKAEDLDLPE 279

RESULT 6
ID 004108_ORYSA PRELIMINARY; PRT; 276 AA.
AC 004108;
DT 01-JUL-1997, integrated into UniProtKB/TrEMBL.
DT 01-JUL-1997, sequence version 1.
DT 07-FEB-2006, entry version 37.
DE Myb factor.
GN Name=myb; Synonyms=OSUNBa0055P24.4;
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
OC Ehrharioideae; Oryzaceae; Oryza.
OX NCBI_TaxId=4530;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=coleoptiles;
RX MEDLINE=97375319; PubMed=9235602;
RA Lu Y.-P., Zhen R.-G., Rea P.A.;
RA "Acrt4; a fourth member of the Arabidopsis phosphate transporter gene
RT family.";
RL (et) Plant Gene Register PCR97-082.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Jenkins C.N., Burr P.C.,
RA Hestel J., Zismann V., Pei G., Bowman C.L., Fujii C.Y., Vanaken S.E.,
RA Bowman C.L., Craven B., Utecherback T.R., Khalak H., Feldblyum T.V.,
RA Quakebuehn J., White O., Salzberg S.L., Fraser C.M.;
RA Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Buell R.;
RA Submitted (Oct-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
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CC EMBL; Y11550; CAA72185.1; -, mRNA.
DR EMBL; AC037425; AAG13574.1; -, Genomic_DNA.
DR PIR; T03823; T03823.
DR HSSP; P06876; 1GV2.
DR Gtrame; 004108; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0045449; F:regulation of transcription; IEA.
DR InterPro; IPR012287; Homodomain-rel.
DR InterPro; IPR01005; MYB_DNA_Bd.
DR Pfam; PF00249; MYB_DNA-binding; 2.
DR SMART; SM00717; SANT; 2.
DR PROSITE; PS00037; MYB_1; UNKNOWN_1.
DR PROSITE; PS00334; MYB_2; UNKNOWN_1.
DR PROSITE; PS00390; MYB_3; 2.
DR DNA-binding; Nuclear protein; Repeat.
SQ SEQUENCE 276 AA; 30065 MW; 45037ADE557CF25 CRC64;

Query Match 51.0%; Score 697.5; DB 2; Length 276;
Best Local Similarity 53.2%; Pred. No. 1.4e-43;
Matches 150; Conservative 34; Mismatches 61; Indels 37; Gaps 10;

QY 1 MGRAPCCCKMGLKKGPMTPPEEDKVLVAHIQRHGHGNWRALPKOAGILRCGSKCRLRWNY 60
DB 1 MGRAPCCCKMGLKKGPMTPPEEDKVLVAHIQRHGHGNWRALPKOAGILRCGSKCRLRWNY 60
QY 61 LRPDIKRGNFSEEDDTIHLHELLGNRWSAIAARLPGRTDNEIKVWHTLKKRLD-- 117
DB 61 LRPDIKRGNFSEEDDTIHLHELLGNRWSAIAARLPGRTDNEIKVWHTLKKRLD-- 120
QY 118 --APAQGGHVAASGGK--HKPKSAKPPAA--AAPASPERSA--SSVSSMA 167
DB 121 KLAAGGG--GRRRPHTRKOPPAKSAKATPSVDTSSTGTCSTVSS--P 174
QY 168 SVAEHNAGISASASVCAKESSFTSASE-----EFOIDSFWSSET--LS 213
DB 175 SSADGDHRRQOQOQTHAAV---KESSFGGELPAAAAAPTAAMDESFWSSTVETGM 231
QY 214 MPLDGYDVSME-PGDAFVAAPSADMDYWLGVFMESGEGADLPQ 254
DB 232 AGLGDMDEELAIAGTSSAAARSDDMEFWLKKLLSGWRDL 273

RESULT 7
ID Q7XDC7_ORYSA PRELIMINARY; PRT; 276 AA.
AC Q7XDC7;
DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2003, sequence version 1.
DT 07-FEB-2006, entry version 22.
DE Myb factor.
GN ORFNames=LOC_Os10g33810;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
OC Ehrharioideae; Oryzaceae; Oryza.
OX NCBI_TaxId=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q., Ouyang S.;
RA Submitted (May-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
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CC EMBL; AB016939; AAP54284.1; -, Genomic_DNA.
DR HSSP; P06876; 1GV2.
DR Gtrame; Q7XDC7; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.

```

DR GO; GO:0045449; P:regulation of transcription; IEA.
 DR InterPro; IPR012287; Homeodomain-rel.
 DR Pfam; PF00249; Myb_DNA-binding_2.
 DR SMART; SM00717; SANT_2.
 DR PROSITE; PS00037; MYB_1; UNKNOWN_1.
 DR PROSITE; PS00334; MYB_2; UNKNOWN_1.
 DR PROSITE; PS00090; MYB_3; 2.
 KW DNA-binding; Nuclear protein; Repeat.
 SO SEQUENCE 276 AA; 3005 MW; 45037ADE5557CF25 CRC64.

Query Match 51.0%; Score 697.5; DB 2; Length 276;
 Best Local Similarity 53.2%; Pred. No. 1.4e-43;
 Matches 150; Conservative 34; Mismatches 61; Indels 37; Gaps 10;

ID	Q9SLTO_TOBAC	PRELIMINARY; PRT; 281 AA.
DT	01-MAY-2000, integrated into UniProtKB/TrEMBL.	
DT	01-MAY-2000, sequence version 1.	
DT	07-FEB-2006, entry version 30.	
DE	Myb-related transcription factor LBM4.	
GN	Name=Lbm4;	
OS	Nicotiana tabacum (Common tobacco).	
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
OC	Spermatophytes; Magnoliophyta; eudicotyledons; core eudicotyledons;	
OC	asterids; lamiales; Solanales; Solanaceae; Nicotiana.	
OX	NCBI_TaxID=4097;	
RN	[1]	
RP	NUCLEOTIDE SEQUENCE.	
RX	MEDLINE=21066940; PubMed=11148294; DOI=10.1105/ltpc.12.12.2511;	
RA	Shigemoto K., Takeda S., Hirochika H.;	
RT	"MYB-related transcription factor NtMYB2 induced by wounding and	
RT	elicitors is a regulator of the tobacco retrotransposon Tto1 and	
RT	defense-related genes".	
RL	Plant Cell 12:2511-2528(2000).	
CC	-1- SUBCELLULAR LOCATION: Nuclear (By similarity).	
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms	
CC	Distributed under the Creative Commons Attribution-NoDerivs License	
DR	EMBL; AB028652; BAA88224.1; -, mRNA.	
DR	HSSP; P06676; 1GV2.	
DR	TRANSFAC; T05251; -.	
DR	GO; GO:0005634; C:nucleus; IEA.	
DR	GO; GO:0003677; F:DNA binding; IEA.	
DR	GO; GO:0045449; P:regulation of transcription; IEA.	
DR	InterPro; IPR012287; Homeodomain-rel.	
DR	InterPro; IPR001005; Myb_DNA_bd.	
DR	Pfam; PF00249; Myb_DNA-binding_2.	
DR	SMART; SM00717; SANT_2.	

Query Match 50.7%; Score 694; DB 2; Length 281;
 Best Local Similarity 49.2%; Pred.No.2,6e-43;
 Matches 147; Conservative 35; Mismatches 55; Indels 62; Gaps 10;

DR PROSITE; PS00037; MYB_1; UNKNOWN_1.
 DR PROSITE; PS00334; MYB_2; 1.
 DR PROSITE; PS50090; MYB_3; 2.
 KM DNA-binding; Nucleat protein; Repeat.
 SQ SEQUENCE 281 AA; 32029 MW; 715FBC9798238625 CRC64;

QY 1 MGRAPCECKGLKKGPPTPEEDKYLVAHIQRHGHGNRRALPKOAGLLRCCKSCSLRWITNY 60
 Db 1 MVRAPCECKKGLKKGPPTPEEDQVLSVYIQTNGGNRRALPKAGLLRCCKSCSLRWITNY 60
 QY 61 LRPPIKCGNFSKEEDPTIHLHELGRGMAIARLPGRTDNEIKVNHHLTKRLDAPA 120
 Db 61 LRPPIKCGNFTREEDSIIQLHEHLGNRMAIARLPGRTDNEIKVNHHLTKRLKRL--- 117
 QY 121 QCGHVAASGCKKPKPR-SAKKPAA-----AAAPASPERSASSSV 161
 Db 118 --NYQPPQNSKSKSNLDSKAPSTQTFNNSDNFNSIOEDINGPVTPGPSQKSS--- 171
 QY 162 TESSMASVABEHNMATISSASAVCAKESSEF-----TSASEEF--QIDDSFMSSETLS- 213
 Db 172 --SEMSVTVTLD-----STAMTTITTDQNMFKQLDENKSSSEFIREIDESFWTNDLST 222
 QY 214 ----MBLDD-----YDVSMEPGDAFYAPSPADMDMYLGVFMESGEAODLPQ 256
 Db 223 GDNSNFMPEMGTEGLQVQPFSSVKGESMD-MVGTKLDEDDMFVYNYVFIKSGDLLDPE 280

RESULT 9
 Q9SLT2_TOBAC PRELIMINARY; PRT; 281 AA.
 ID Q9SLT2_TOBAC
 AC Q9SLT2;
 DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
 DT 01-MAY-2000, sequence version 1.
 DT 07-FEB-2006, entry version 29.
 DE MYB-related transcription factor LBM1.
 GN Name=Lbm1;
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC Asterids; Lamiales; Solanales; Solanaceae; Nicotiana.
 CX NCBI_TaxId=4097;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21066940; Pubmed=11148294; DOI=10.1105/tpc.12.12.2511;
 RA Sugimoto K., Takeda S., Hirochika H.;
 RT "MYB-related transcription factor NMY2 induced by wounding and
 RT elicitors is a regulator of the tobacco retrotransposon Tto1 and
 RT defense-related genes.";
 RL Plant Cell 12:2511-2528(2000).
 CC -!- SUBCELLULAR LOCATION: Nucleat (By similarity).
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CC EMBL; AB028649; BAA8221.1; -; Genomic_DNA.
 DR HSSP; P06876; 1GV2.
 DR TRASNSEC; T05245; -.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0045449; P:regulation of transcription; IEA.
 DR InterPro; IPR012287; Homeodomain-rel.
 DR InterPro; IPR001005; Myb_DNA_bd.
 DR Pfam; PF00249; Myb_DNA-binding; 2.
 DR SMART; SM00717; SANT; 2.
 DR PROSITE; PS00037; MYB_1; UNKNOWN_1.
 DR PROSITE; PS00334; MYB_2; 1.
 DR PROSITE; PS50090; MYB_3; 2.
 KM DNA-binding; Nucleat protein; Repeat.
 SQ SEQUENCE 281 AA; 31985 MW; 0EB07C4900A5522A CRC64;

KM DNA-binding; Nuclear protein; Repeat.
 SQ SEQUENCE 277 AA; 32076 MW; D4FD3FB2B1252885 CRC64;
 Query Match 50.0%; Score 684; DB 2; Length 277;
 Best Local Similarity 48.2%; Pred. NO. 1,4e-42;
 Matches 144; Conservative 37; Mismatches 52; Indels 66; Gaps 10;

QY 1 MGRAPCECKMKGLKGPWTPEDKVLVAHIQRHGNMRLPKOAGLRCCKSRLRWINY 60
 |||||
 DB 1 MGRAPCECKMKGLKGPWTPEDQILSYIQNGHGNRALPKOAGLRCCKSRLRWINY 60
 |||||
 QY 61 LRDPDKRGNFSKEEDDTIHLHLLGNRMSAIAARLPGRDNEIKVNMHTLKKRLDPA 118
 |||||
 DB 61 LRDPDKRGNFTKEEDDTIHLHLLGNRMSAIAAKLPGRDNEIKVNMHTLKKRLDPA 120
 |||||
 QY 119 PAQGGHVAASGGKHKKPKAKKPAAPAAAAA-----PPASPERAS 158
 |||||
 DB 121 PPG-----NPKRHSKNHDSKGPSTSSNNSHLFTYQKHIDSSVPAPNSPQISS 173
 |||||
 QY 159 SSVTESSMASSVAEHNAGISSASVCAKESSFTSASEF-QIDDSFMSSETLMP-- 215
 |||||
 DB 174 ---TEMSTVTLV-DDH-----QWIKQEE--MESSEYPEIDESFTWTKLSTDN 217
 |||||
 QY 216 -LDGYVSMERPCA-----FVAPPSADMDYWLGVFMESGEAODLPQ 256
 |||||
 DB 218 WSNTHDHVMTADQELQVLPFSSLKENVDMLTTRKEDMDRMVNVFRTDLPPELPE 276
 |||||

RESULT 12
 0987E3 SOYBN PRELIMINARY; PRT; 264 AA.
 ID 0987E3 SOYBN
 AC 0987E3
 DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
 DT 01-MAY-2000, sequence version 1.
 DT 07-FEB-2006, entry version 27.
 DE GmMYB29A1 protein.
 GN Name=GmMYB29A1;
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 OC Glycine.
 NCBI_TaxID=3847;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Shimizu T., Fujibe R., Senda M., Ishikawa R., Harada T., Niizeki M.,
 RA Akada S.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC
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 CC
 CC EMBL; AB029160; BAA81731.1; -; Genomic DNA.
 CC EMBL; AB029159; BAA81730.1; -; Genomic DNA.
 CC HSSP; P06876; 1GVD.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0045449; P:regulation of transcription; IEA.
 DR InterPro; IPR012287; Homeodomain-rel.
 DR InterPro; IPR01005; MYB DNA bd.
 DR Pfam; PF00249; MYB DNA-binding; 2.
 DR SMART; SM00717; SANT; 2.
 DR PROSITE; PS00037; MYB_1; UNKNOWN_1.
 DR PROSITE; PS00334; MYB_2; 1.
 DR PROSITE; PS50090; MYB_3; 2.
 KM DNA-binding; Nuclear protein; Repeat.
 SQ SEQUENCE 264 AA; 30387 MW; A2B710AFECAB66A CRC64;
 Query Match 49.5%; Score 677.5; DB 2; Length 264;
 Best Local Similarity 48.4%; Pred. NO. 4.1e-42;
 Matches 138; Conservative 39; Mismatches 57; Indels 51; Gaps 6;

QY 1 MGRAPCECKMKGLKGPWTPEDKVLVAHIQRHGNMRLPKOAGLRCCKSRLRWINY 60
 |||||
 DB 1 MGRAPCECKMKGLKGPWTPEDQILMSYIQNGHGNRALPKOAGLRCCKSRLRWINY 60
 |||||
 QY 61 LRDPDKRGNFSKEEDDTIHLHLLGNRMSAIAARLPGRDNEIKVNMHTLKKRLDAPA 120
 |||||
 DB 61 LRDPDKRGNFSSEEDDTIHLHLLGNRMSAIAAKLPGRDNEIKVNMHTLKKRLDAPA 116
 |||||
 QY 121 QGGHVAASGGKHKKPKAKKPAAPAAAAAAPPASPERASSSVTESSMASSVAEHNAGIS 180
 |||||
 DB 117 ---NNSDNTKRVSKPRIRKSDNSSTLTQSEP--TSSGCTTSSDPSSFSFE-----G 163
 |||||
 QY 181 SASASVCAKESSFTSASEFOIDDSFW-----SETLSMPLDGYVSMERPCA-FVAP 232
 |||||
 DB 164 TKMDNMNTRKEDIENETKPPIDESFWPOETVDYSSSTMOSNSMTISNE-----LAP 218
 |||||
 QY 233 PS-----ADMDYWLGVFMESGEAODLPQ 256
 |||||
 DB 219 PQYQFNSVETPQQQSVGVNDSKFDQDMDFWYDIFIKSGSIELPE 263
 |||||

RESULT 13
 P93391 TOBAC PRELIMINARY; PRT; 278 AA.
 ID P93391 TOBAC
 AC P93391
 DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.
 DT 01-MAY-1997, sequence version 1.
 DT 07-FEB-2006, entry version 34.
 DE Transcription factor Myb1 (Myb-related transcription factor LBM3).
 GN Name=myb1; Synonyms=Lbm3;
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC asterids; lamids; Solanales; Solanaceae; Nicotiana.
 NCBI_TaxID=4997;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Xanthi nc;
 RX MEDLINE=97121500; PubMed=8962166; DOI=10.1073/pnas.93.25.14972;
 RA Yang Y., Kleesig D.F.;
 RT "Isolation and characterization of a tobacco mosaic virus-inducible
 RT myb oncogene homolog from tobacco."
 RL Proc. Natl. Acad. Sci. U.S.A. 93:14972-14977 (1996).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Yang Y., Kleesig D.F.;
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA Sugimoto K., Hirochika H.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC
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 CC
 CC EMBL; U72762; AAB41101.1; -; mRNA.
 CC EMBL; AB028651; BAA88223.1; -; mRNA.
 CC PIR; T03850; T03850.
 CC HSSP; P06876; 1MBK.
 DR TRANSFAC; T02880; -.
 DR TRANSFAC; T05250; -.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0045449; P:regulation of transcription; IEA.
 DR InterPro; IPR012287; Homeodomain-rel.
 DR InterPro; IPR01005; MYB DNA bd.
 DR Pfam; PF00249; MYB DNA-binding; 2.
 DR SMART; SM00717; SANT; 2.
 DR PROSITE; PS00037; MYB_1; UNKNOWN_1.
 DR PROSITE; PS00334; MYB_2; 1.
 DR PROSITE; PS50090; MYB_3; 2.
 KM DNA-binding; Nuclear protein; Repeat.

Seq	Sequence	278 AA	32005 MW	16090D1911B74E572 CRC64
Qy	Query Match	48.9%	Score 669.5	DB 2; Length 278;
Beet	Local Similarity	47.2%	Pred. No. 1.7e-41;	
Matches	141; Conservative	37;	Mismatches 56;	Indels 65; Gaps 10;
Db	1 MGRAPCCCKMGLKKGPMTPEDDKVIVAHIQRHGHGNWRAALPKQAGLLRCGKSCRIRWNY	60		
Qy	1 LRPDIKRNFSKEEEDTIIHLHELGNWSAIAARLPGRTNENIGVWHTLKKRLD--A	118		
Db	61 LRPDIKRNFTKEEETIIQLHEMLGNRWSAIAALPRTDNEIGNVWHTLKKTLKDYK	120		
Qy	119 PAQGVAAASGGKKKKKKRS--AKKPAAAAA-----APPASPERSAASS	160		
Db	121 PPO-----NSKRHSKSKNDHKSPTTSSSSNNDLTIINTQKHIDSPVLAIPNSPOISS	173		
Qy	161 VTSSMASSVAEHHNAGISSASAVCKKEESSFTPSASEEF-QIDPSWSETLS-----	213		
Db	174 STEMSTVLV-DH-----QNVVVKQF--VNESSEYPELIDESTWTDLTLDNNKS	221		
Qy	214 -----MPLDGYDVSMEPGDAFAPPSADDMNDYMLGVFMESGEADLPQ	256		
Db	222 STDHVAANAQELQVLPFSSF---KEENVLDLATKMDMDMFYVNFVIKTDIDLPPELB	277		
RESULT 14				
ID	09XIU9_SOYBN	PRELIMINARY;	PRT;	264 AA.
AC	09XIU9;			
DT	01-NOV-1999, integrated into UniProtKB/TrEMBL.			
DT	01-NOV-1999, sequence version 1.			
DT	07-FEB-2006, entry version 32.			
DE	GmMYB29A2 protein.			
GN	Name=GmMYB29A2;			
OS	Glycine max (Soybean).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;			
OC	rosids; eustroids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;			
OC	Glycine.			
OX	NCBI_TaxID=3847;			
RN	(1)			
RP	NUCLEOTIDE SEQUENCE.			
RA	Shinizu T., Fujide R., Senda M., Ishikawa R., Harada T., Nizeki M.,			
RA	Akada S.;			
RL	Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.			
CC	-1- SUBCELLULAR LOCATION: Nuclear (By similarity).			
CC	-----			
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms			
CC	Distributed under the Creative Commons Attribution-NonCommercial license			
CC	-----			
DR	EMBL; AB029161; BAA61732.1; -; Genomic_DNA.			
DR	HSSP; P06876; LGVD.			
DR	GO; GO:0005634; C:nucleus; IEA.			
DR	GO; GO:0003677; F:DNA binding; IEA.			
DR	GO; GO:0045449; P:regulation of transcription; IEA.			
DR	InterPro; IPR012287; Homeodomain-tel.			
DR	InterPro; IPR010005; MYB DNA Bd.			
DR	Pfam; PF00249; MYB DNA-Binding; 2.			
DR	SMART; SM00717; SMT; 2.			
DR	PROSITE; PS00037; MYB_1; UNKNOWN_1.			
DR	PROSITE; PS00334; MYB_2; 1.			
DR	PROSITE; PS50090; MYB_3; 2.			
KW	DNA-binding; Nuclear protein; Repeat.			
SO	SEQUENCE 264 AA; 30201 MW; ADE2BI192ABB63780 CRC64;			
Query Match	48.6%	Score 665.5	DB 2; Length 264;	
Beet Local Similarity	46.7%	Pred. No. 3.1e-41;		
Matches	142; Conservative	33;	Mismatches 38;	Indels 91; Gaps 8
Qy	1 MGRAPCCCKMGLKKGPMTPEDDKVIVAHIQRHGHGNWRAALPKQAGLLRCGKSCRIRWNY	60		

Dr Db 1 MRAPRCCCKMKGLKGGWTPBEDQILMSYI QKHGHGNMBAFLRKLGLRLCGSKSCLRWINY 60

Qy 61 LRPDIRGNFNSKEEDDTIITHELLIGNRWSAIAARLPRTDNEIKNWHHTLKKRLDAPA 120

Db 61 LRPDIRGNFNSSEEBEIIIKHHELLGNRWSAIAARLPRTDNEIKNWHHTLKKRL 110

Qy 121 QGGHVAASGGKHKKRSKSAKKDPAAPAPAPPERKSASSVTESSMASSVAEEHGNAGIS 180

Db 117 ----LMSDIOKRKSKRT-----KSDSNSSTLTL 14

Qy 181 SASAVCAKEESSFTSASEFO-----IDDFNSE-----TLS 213

Db 144 EPTSSACTSLSPDSSFSSEGTQKMDNMKISDIESVETIMPEPIDESFMSKATVDYESTM 203

Qy 214 MPDGDYDVSNRPDVAARP-----SADD---MRYMVGVMESGEA 25

Db 204 MTNSMTSTISNE-----LAPPOYQFNSVESFOQOQSVYNGSDHDDGMDFWDFIKSGES 258

Qy 252 QDLP 255

Db 259 IEUP 262

RESULT 15

Q9LTC4 ARATH PRELIMINARY; PRT; 285 AA.

AC 09LTC4;

DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.

DT 01-OCT-2000, sequence version 1.

DT 07-FEB-2006, entry version 29.

DE MYB-related transcription factor (MYB transcription factor).

GN OrderedLocustNames=At3g23250;

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eucosida II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID=3702;

RA NP MEDLINE=20277480; PubMed=10819329; DOI=10.1093/dnares/7.2.131;

RX Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Tabata S.;

RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence features of the regions of 4,504,864 bp covered by sixty P1 and TAC clones";

RL DNA Res. 7:131-135(2000).

RA NP NUCLEOTIDE SEQUENCE.

RP Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;

RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.

RA NP [3]

RP NUCLEOTIDE SEQUENCE.

RL Qu L., Gu H.;

RA Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.

RA NP [4]

RP NUCLEOTIDE SEQUENCE.

RA Tsuchi Y., Seki M., Ishida J., Nakajima M., Enju A., Kamiya A.,

RA Natusaka M., Shun-I T., Nakagawa M., Sakamoto N., Oishi K., Kohara Y.,

RA Satou M., Toyoda T., Konagaya A., Sakaki Y., Sekurai T., Iida K., Akiyama K.,

RA Hayashizaki Y., Shinozaki K.;

RT "Large-scale analysis of RIKEN Arabidopsis full-length (RAFL) cDNAs";

RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.

CC -I- SUBCELLULAR LOCATION: Nuclear (By similarity).

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CC EMBL: AB025608; BAA95738.1; -; Genomic_DNA.

DR EMBL: AY550296; AAS58507.1; -; mRNA.

DR EMBL: AKI76617; BAD44380.1; -; mRNA.

DR EMBL: AKI76693; BAD44456.1; -; mRNA.

DR HSSP: P06876; 1GV2.

DR TAIR: At3g23250; -.

DR GO: GO:0005634; C:nucleus; IEA.
DR GO: GO:0003577; F:DNA binding; IEA.
DR GO: GO:0045449; P:regulation of transcription; IEA.
DR InterPro: IPR012287; Homeodomain-rel.
DR InterPro: IPR001005; Myb DNA bd.
DR Pfam: PF00249; Myb DNA-binding; 2.
DR SMART: SM00717; SANT; 2.
DR PROSITE: PS00037; MYB_1; UNKNOWN_1.
DR PROSITE: PS00334; MYB_2; 1.
DR PROSITE: PS50090; MYB_3; 2.
KW DNA-binding; Nuclear protein; Repeat.
SQ SEQUENCE 285 AA; 32042 MW; 51CEFC6DF50F828 CRC64;

Query Match 48.4%; Score 661.5; DB 2; Length 285;
Best Local Similarity 49.0%; Pred. No. 6,9e-41;
Matches 146; Conservative 25; Mismatches 66; Indels 61; Gaps 6;
QY 1 MGRAPCCCEKMKLKKGPWTPPEEDKVLVAHIQRHGHNRRALPKOAGLLRCGKSCRLRWINY 60
DB 1 MGRAPCCCEKMKLKKGPWTPPEEDQILVSFILNHGSHNRALPKOAGLLRCGKSCRLRWINY 60
QY 61 LRPDIKRGNFSEKEEDTIIHLHELGNRWSAIAARLPGRTDNEIKVWHTHLKKRLDAPA 120
DB 61 LRPDIKRGNFTEEDDAIISLHQLGNRWSAIAAKLPGRTDNEIKVWHTHLKKRLDAPY 119
QY 121 QCGHVAASGCKKKPKRSAKKPAAAAAAPASPERASSSVTESSMASSVAEEHGNAGIS 180
DB 120 QPAKPKTSNKKKGTGTPKS-----ESVITSSNSTRSESELADS----SNPAGES 163
QY 181 SASASYCAKESSSFTSASE-----FQIDDFWSET 211
DB 164 LRFTSPSTSEVSSMTLSHDGYSNEINMDNKPQDISTITDQCVSFETFGADIDSEFWKET 223
QY 212 LSNPLDGYDVS-----MEPGDAFYAPPSAD-----DMDYWLGVFMESGEAODL 254
DB 224 LYSQDEHNYSNLEVAGLVEIQOEFONLGSANNEMI FDSEMDFWFDVLARTGGEODL 281

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